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NEWS 3 JUN 01 CAS REGISTRY Source of Registration (SR) searching enhanced on STN
NEWS 4 JUN 26 NUTRACEUT and PHARMAML no longer updated
NEWS 5 JUN 29 IMSCOPROFILE now reloaded monthly
NEWS 6 JUN 29 EPFULL adds Simultaneous Left and Right Truncation (SLART) to AB, MCLM, and TI fields
NEWS 7 JUL 09 PATDPAFULL adds Simultaneous Left and Right Truncation (SLART) to AB, CLM, MCLM, and TI fields
NEWS 8 JUL 14 USGENE enhances coverage of patent sequence location (PSL) data
NEWS 9 JUL 27 CA/CAplus enhanced with new citing references
NEWS 10 JUL 16 GBFULL adds patent backfile data to 1855
NEWS 11 JUL 21 USGENE adds bibliographic and sequence information
NEWS 12 JUL 28 EPFULL adds first-page images and applicant-cited references
NEWS 13 JUL 28 INPADOCDB and INPAFAMDB add Russian legal status data
NEWS 14 AUG 10 Time limit for inactive STN sessions doubles to 40 minutes
NEWS 15 AUG 18 COMPENDEX indexing changed for the Corporate Source (CS) field
NEWS 16 AUG 24 ENCOMPLIT/ENCOMPLIT2 reloaded and enhanced
NEWS 17 AUG 24 CA/CAplus enhanced with legal status information for U.S. patents
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=> s (array# or microarray#)/bi,ab 211941 ARRAY#/BI
196938 ARRAY#/AB 75584 MICROARRAY#/BI
45394 MICROARRAY#/AB
L1 271500 (ARRAY# OR MICROARRAY#)/BI,AB

=> s ((duplicat? or replicat? or repeat?)(30a)((oligo(w)nucle?) or oligonucle? or odn#))/bi,ab 43212 DUPLICAT?/BI
40828 DUPLICAT?/AB 161916 REPLICAT?/BI
148151 REPLICAT?/AB 388568 REPEAT?/BI
370979 REPEAT?/AB 30285 OLIGO/BI
15021 OLIGO/AB 2297139 NUCLE?/BI
1328727 NUCLE?/AB 103027 OLIGONUCLE?/BI
76625 OLIGONUCLE?/AB 5299 ODN#/BI
5106 ODN#/AB

L2 2485 ((DUPLICAT? OR REPLICAT? OR REPEAT?)(30A)((OLIGO(W)NUCLE?) OR OLIGONUCLE? OR ODN#))/BI,AB

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=> s l1 and l2
L3 234 L1 AND L2

=> s l3 not 2009/py 1212953 2009/PY
L4 213 L3 NOT 2009/PY

=> s l4 not 2008/py 1758525 2008/PY
L5 181 L4 NOT 2008/PY

=> s l5 not 2007/py 1714883 2007/PY
L6 153 L5 NOT 2007/PY

=> s l6 not 2006/py 1584042 2006/PY
L7 127 L6 NOT 2006/PY

=> s l7 not 2005/py 1431439 2005/PY
L8 111 L7 NOT 2005/PY

=> s l8 not 2004/py 1349873 2004/PY
L9 93 L8 NOT 2004/PY

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(FILE 'HOME' ENTERED AT 19:19:56 ON 21 SEP 2009)
FILE 'CAPLUS' ENTERED AT 19:20:27 ON 21 SEP 2009
L1 271500 S (ARRAY# OR MICROARRAY#)/BI,AB
L2 2485 S ((DUPLICAT? OR REPLICAT? OR REPEAT?)(30A)((OLIGO(W)NUCLE?) OR
L3 234 S L1 AND L2
L4 213 S L3 NOT 2009/PY
L5 181 S L4 NOT 2008/PY
L6 153 S L5 NOT 2007/PY
L7 127 S L6 NOT 2006/PY
L8 111 S L7 NOT 2005/PY
L9 93 S L8 NOT 2004/PY

=> d l9 1-93 bib ab

L9 ANSWER 1 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:43508 CAPLUS <<LOGINID::20090921>>
DN 143:1790
TI Model-based analysis of oligonucleotide ***arrays*** and issues in cDNA ***microarray*** analysis
AU Li, Cheng; Tseng, George C.; Wong, Wing Hung
CS Department of Biostatistics, Harvard School of Public Health, Boston, MA, USA
SO Statistical Analysis of Gene Expression Microarray Data (2003), 1-34,201-211. Editor(s): Speed, Terry. Publisher: Chapman & Hall, Boca Raton, Fla. CODEN: 69GJTB; ISBN: 1-58488-327-8
DT Conference
LA English
AB The model-based anal. of ***oligonucleotide*** ***arrays*** is described, including expression index computation, outlier detection, and std. error applications, as well as issues in the anal. of cDNA ***array*** data such as normalization, handling of ***replicate*** ***arrays*** and spots, and hierarchical modeling of the data in detecting differentially expressed genes. Software implementing these anal. methods can be found at http://biosun1.harvard.edu/complab/.
RE.CNT 239 THERE ARE 239 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:885512 CAPLUS <<LOGINID::20090921>>
DN 142:50107
TI DNA chip manufacturing method
IN Kim, Su Hyeon; Kim, Tae Han; Lee, Gang Sin; Lee, Won Yong; Park, Je Gyun
PA Lg Electronics Inc., S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, No pp. given
CODEN: KRXXA7
DT Patent
LA Korean
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI KR 2001036009 A 20010507 KR 1999-42841 19991005
PRAI KR 1999-42841 19991005
AB A method for manufg. a DNA chip is provided to duplicate a plurality of DNA chips with a single DNA chip, thereby achieving mass-prodn. of the DNA chip in a simplified process at a low cost. A method for manufg. a DNA chip includes the steps of prepg. a source substrate bonded with different kinds of oligo nucleic acid and a soln. mixed with DNA pieces able to be bond with oligo nucleic acid compatibly, immersing the source substrate into the soln. for bonding the DNA pieces to corresponding oligo nucleic acid compatibly, positioning a target substrate on the DNA pieces compatibly bonded with the corresponding ***oligo*** ***nucleic*** acid, breaking the compatible bond of the DNA pieces and bonding the broken DNA pieces to the target substrate, and ***repeating*** the 2nd to 4th steps in sequence.

L9 ANSWER 3 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:10282 CAPLUS <<LOGINID::20090921>>
DN 140:178641
TI Transcriptional profiling of epidermal keratinocytes: Comparison of genes expressed in skin, cultured keratinocytes, and reconstituted epidermis, using large DNA ***microarrays***
AU Gazel, Alix; Ramphal, Patricia; Rosdy, Martin; De Wever, Bart; Tornier, Carine; Hosein, Nadia; Lee, Brian; Tomic-canic, Marjana; Blumenberg, Miroslav
CS Department of Dermatology, New York University School of Medicine, New York, USA
SO Journal of Investigative Dermatology (2003), 121(6), 1459-1468 CODEN: JIDEAE; ISSN: 0022-202X
PB Blackwell Publishing, Inc.
DT Journal
LA English
AB Epidermal keratinocytes are complex cells that create a unique three-dimensional (3-D) structure, differentiate through a multistage process, and respond to extracellular stimuli from nearby cells. Consequently, keratinocytes express many genes, i.e., have a relatively large "transcriptome.". To det. which of the expressed genes are innate to keratinocytes, which are specific for the differentiation and 3-D architecture, and which are induced by other cell types, the authors compared the

transcriptomes of skin from human subjects, differentiating 3-D reconstituted epidermis, cultured keratinocytes, and nonkeratinocyte cell types. Using large ***oligonucleotide*** ***microarrays*** , the authors analyzed five or more ***replicates*** of each, which yielded statistically consistent data and allowed identification of the differentially expressed genes. Epidermal keratinocytes, unlike other cells, express many proteases and protease inhibitors and genes that protect from UV light. Skin specifically expresses a higher no. of receptors, secreted proteins, and transcription factors, perhaps influenced by the presence of nonkeratinocyte cell types. Surprisingly, mitochondrial proteins were significantly suppressed in skin, suggesting a low metabolic rate. Three-dimensional samples, skin and reconstituted epidermis, are similar to each other, expressing epidermal differentiation markers. Cultured keratinocytes express many cell-cycle and DNA replication genes, as well as integrins and extracellular matrix proteins. These results define innate, architecture-specific, and cell-type-regulated genes in epidermis.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:945176 CAPLUS <<LOGINID::20090921>>
DN 140:252120
TI Global profiling of double stranded RNA- and IFN-.gamma.-induced genes in rat pancreatic beta cells
AU Rasschaert, J.; Liu, D.; Kutlu, B.; Cardozo, A. K.; Kruhoffer, M.; Ortoft, T. F.; Eizirik, D. L.
CS Laboratory of Experimental Medicine, Universite Libre de Bruxelles, Brussels, 1070, Belg.
SO Diabetologia (2003), 46(12), 1641-1657 CODEN: DBTGAJ; ISSN: 0012-186X
PB Springer-Verlag
DT Journal
LA English
AB Aims/hypothesis. Viral infections and local prodn. of IFN-.gamma. might contribute to beta-cell dysfunction/death in Type 1 Diabetes. Double stranded RNA (dsRNA) accumulates in the cytosol of viral-infected cells, and exposure of purified rat beta cells to dsRNA (tested in the form of polyinosinic-polycytidylic acid, PIC) in combination with IFN-.gamma. results in beta-cell dysfunction and apoptosis. To elucidate the mol. mechanisms involved in PIC + IFN-.gamma.-effects, we detd. the global profile of genes modified by these agents in primary rat beta cells. Methods. FACS-purified rat beta cells were cultured for 6 or 24 h in control condition or with IFN-.gamma., PIC or a combination of both agents. The gene expression profile was analyzed in ***duplicate*** by high-d. ***oligonucleotide*** ***arrays*** representing 5000 full-length genes and 3000 EST's. Changes of greater than or equal to 2.5-fold were considered as relevant. Results. Following a 6- or 24-h treatment with IFN-.gamma., PIC or IFN-.gamma. and PIC, we obsd. changes in the expression of 51 to 189 genes. IFN-.gamma. modified the expression of MHC-related genes, and also of genes involved in beta-cell metab., protein processing, cytokines and signal transduction. PIC affected preferentially the expression of genes related to cell adhesion, cytokines and dsRNA signal transduction, transcription factors and MHC. PIC and/or IFN-.gamma. up-regulated the expression of several chemokines and cytokines that could contribute to mononuclear cell homing and activation during viral infection, while IFN-.gamma. induced a pos. feedback on its own signal transduction. PIC + IFN-.gamma. inhibited insulin and GLUT-2 expression without modifying pdx-1 mRNA expression. Conclusion/interpretation. This study provides the first comprehensive characterization of the mol. responses of primary beta cells to dsRNA + IFN-.gamma., two agents that are probably present in the beta cell milieu during the course of virally-induced insulitis and Type 1 Diabetes. Based on these findings, we propose an integrated model for the mol. mechanisms involved in dsRNA + IFN-.gamma. induced beta-cell dysfunction and death.
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)
RE.CNT 90 THERE ARE 90 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:740299 CAPLUS <<LOGINID::20090921>>
DN 139:359413
TI ***Oligonucleotide*** ***arrays*** for genotyping: enzymatic methods for typing single nucleotide polymorphisms and short tandem ***repeats***
AU Case-Green, Stephen; Pritchard, Clare; Southern, Edwin
CS Department of Biochemistry, University of Oxford, Oxford, UK
SO Methods in Molecular Biology (Totowa, NJ, United States) (2003), 226(PCR Protocols (Second Edition)), 255-269 CODEN: MMBIED; ISSN: 1064-3745
PB Humana Press Inc.
DT Journal
LA English
AB The fabrication and some uses of oligonucleotide ***arrays*** and the flexibility of the ***array*** platform are discussed. Analytic methods for measurement of single nucleotide polymorphisms (SNPs) and short tandem repeats (STR) are presented. Three broad classes of assays useful with oligonucleotide ***arrays*** are described: allele-specific hybridization, primer extension by polymerase (minisequencing) and ligase assay.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 6 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:734565 CAPLUS <<LOGINID::20090921>>
DN 139:346487
TI Congruence of tissue expression profiles from gene expression Atlas, SAGEmap and TissueInfo databases
AU Huminiecki, Lukasz B.; Lloyd, Andrew T.; Wolfe, Ken
CS Dep. of Genetics, Smurfit Inst., University of Dublin, Trinity College, Dublin, Ire.
SO BMC Genomics (2003), 4, No pp. given CODEN: BGMEET; ISSN: 1471-2164 URL: http://www.biomedcentral.com/1471-2164/4/31
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Extg. biol. knowledge from large amts. of gene expression information deposited in public databases is a major challenge of the postgenomic era. Addnl. insights may be derived by data integration and cross-platform comparisons of expression profiles. However, database meta-anal. is complicated by differences in exptl. technologies, data post-processing, database formats, and inconsistent gene and sample annotation. We have analyzed expression profiles from three public databases: Gene

Expression Atlas, SAGEmap and TissueInfo. These are repositories of oligonucleotide ***microarray*** , Serial Anal. of Gene Expression and Expressed Sequence Tag human gene expression data resp. We devised a method, Preferential Expression Measure, to identify genes that are significantly over- or under-expressed in any given tissue. We examd. intra- and inter-database consistency of Preferential Expression Measures. There was good correlation between ***replicate*** expts. of ***oligonucleotide*** ***microarray*** data, but there was less coherence in expression profiles as measured by Serial Anal. of Gene Expression and Expressed Sequence Tag counts. We investigated inter-database correlations for six tissue categories, for which data were present in the three databases. Significant pos. correlations were found for brain, prostate and vascular endothelium but not for ovary, kidney, and pancreas. We show that data from Gene Expression Atlas, SAGEmap and TissueInfo can be integrated using the UniGene gene index, and that expression profiles correlate relatively well when large nos. of tags are available or when tissue cellular compn. is simple. Finally, in the case of brain, we demonstrate that when PEM values show good correlation, predictions of tissue-specific expression based on integrated data are very accurate.
RE.CNT 86 THERE ARE 86 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 7 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:646413 CAPLUS <<LOGINID::20090921>>
DN 139:287168
TI Structure-function relationships in nucleosomal ***arrays*** containing linker histone H5
AU Sanchez, Miguel A.; Velasco, Lara; Palacian, Enrique
CS Centro de Biologia Molecular "Severo Ochoa", Consejo Superior de Investigaciones Cientificas and Universidad Autonoma de Madrid, Madrid, 28049, Spain
SO Biochimica et Biophysica Acta, Gene Structure and Expression (2003), 1628(3), 177-185 CODEN: BBGSD5; ISSN: 0167-4781
PB Elsevier B.V.
DT Journal
LA English
AB To study the structural and functional changes accompanying the integration of histone H5 into the nucleosome structure, linear DNA species have been employed with a terminal promoter for bacteriophage T7 RNA polymerase followed by tandem repeats of a 207-bp nucleosome positioning sequence. The ***oligonucleosomes*** assembled from 12-***repeat*** DNA and satg. amts. of core histone octamer plus histone H5 are compacted, in the presence of 1 mM free magnesium ions, to the level of the 30-nm fiber. Under these ionic conditions the efficiency in RNA synthesis and the size distribution of RNA chains obtained with this template are the same as those corresponding to the template without H5, indicating that the 30-nm fiber stabilized by H5 does not impair RNA elongation. Therefore, under our exptl. conditions, incorporation of one mol. of histone H5 per nucleosome does not affect elongation of RNA even when a folded structure is produced. However, elongation is inhibited by binding of an excess of H5.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 8 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:566890 CAPLUS <<LOGINID::20090921>>
DN 139:208684
TI Divergence in the spatial pattern of gene expression between human duplicate genes
AU Makova, Kateryna D.; Li, Wen-Hsiung
CS Department of Ecology and Evolution, University of Chicago, Chicago, IL, 60637, USA
SO Genome Research (2003), 13(7), 1638-1645 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB ***Microarray*** gene expression data provide a wealth of information for elucidating the mode and tempo of mol. evolution. In the present study, we analyze the spatial expression pattern of human ***duplicate*** gene pairs by using ***oligonucleotide*** ***microarray*** data, and study the relationship between coding sequence divergence and expression divergence. First, we find a strong pos. correlation between the proportion of duplicate gene pairs with divergent expression (as presence or absence of expression in a tissue) and both synonymous (Ks) and nonsynonymous divergence (KA). The divergence of gene expression between human duplicate genes is rapid, probably faster than that between yeast duplicates in terms of generations. Second, we compute the correlation coeff. (R) between the expression levels of duplicate genes in different tissues and find a significant neg. correlation between R and Ks. There is also a neg. correlation between R and KA, when KA .ltoreq. 0.2. These results indicate that protein sequence divergence and divergence of spatial expression pattern are initially coupled. Finally, we compare the functions of those duplicate genes that show rapid divergence in spatial expression pattern with the functions of those duplicate genes that show no or little divergence in spatial expression.
OSC.G 78 THERE ARE 78 CAPLUS RECORDS THAT CITE THIS RECORD (78 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 9 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:557118 CAPLUS <<LOGINID::20090921>>
DN 139:228272
TI Molecular Phenotype of Spontaneously Arising 4N (G2-Tetraploid) Intermediates of Neoplastic Progression in Barrett's Esophagus
AU Barrett, Michael T.; Pritchard, David; Palanca-Wessels, Corinna; Anderson, Judy; Reid, Brian J.; Rabinovitch, Peter S.
CS Divisions of Human Biology, Fred Hutchinson Cancer Research Center, Seattle, WA, 98104, USA
SO Cancer Research (2003), 63(14), 4211-4217 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Elevated 4N (G2-tetraploid) cell populations are unstable intermediates in the development of many human cancers. However, 4N cell populations are intermixed with larger diploid fractions in vivo, limiting investigation of these key intermediates of neoplastic progression. Therefore, to study elevated 4N cell populations in human neoplasia, we used flow cytometry to purify populations of spontaneously arising TP53wt and TP53mut 4N cells from cell strains derived from premalignant Barrett's esophagus biopsies. Using ***oligonucleotide*** ***arrays*** , we identified 625 genes differentially expressed in at least one ***replicate*** 2N/4N comparison in each strain and in hTERT-immortalized cultures of the TP53mut strains. Strikingly, when hierarchically clustered, these data

contained a large node of 124 genes that were up-regulated in 4N TP53mut cells in the absence of condensed chromosomes. Most of these genes function in G2-M to mediate processes such as chromosome condensation and segregation. These results describe the mol. phenotype of dysregulated G2-M functions and cell cycle checkpoints in a key intermediate of human neoplastic progression.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 10 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:536307 CAPLUS <<LOGINID::20090921>>
DN 139:174326
TI Identification of a nuclear factor kappa B-dependent gene network
AU Tian, Bing; Brasier, Allan R.
CS Department of Medicine and the Sealy Center for Molecular Sciences, The University of Texas Medical Branch, Galveston, TX, 77555-1060, USA
SO Recent Progress in Hormone Research (2003), 58, 95-130 CODEN: RPHRA6; ISSN: 0079-9963
PB Endocrine Society
DT Journal; General Review
LA English
AB A review, with refs. Nuclear factor-kappa B (NF-.vkappa.B) is a highly inducible transcription factor that plays an important role in the hepatic acute-phase response, innate/adaptive immunity, and cellular survival through the induction of genetic networks. The major transcriptional-activating species Rel A-NF-.vkappa.B is a cytoplasmic complex whose nuclear translocation is controlled by its assocn. with a family of inhibitory proteins, termed I.vkappa.Bs. Activation of NF-.vkappa.B results in the targeted proteolysis of I.vkappa.B, releasing NF-.vkappa.B to enter the nucleus and bind to specific sequences in target promoters. Because the genomic actions of NF-.vkappa.B are influenced by the stimulus applied and the promoter context/chromatin structure in which it binds, the spectrum of NF-.vkappa.B-regulated genes has not been elucidated. We have begun to address this question, exploiting a tightly regulated cellular system expressing a nondegradable I.vkappa.B.alpha. mutant that completely inhibits NF-.vkappa.B action. High-d. ***oligonucleotide*** ***microarrays*** were used to identify genetic responses in response to complex biol. stimuli (viral ***replication***) in the presence and absence of NF-.vkappa.B. Using statistical and informatics tools, we identified two groups of NF-.vkappa.B-dependent genes with distinct expression profiles: a group with high constitutive expression whose expression levels fall in response to viral exposure and constitutive mRNA expression increases from NF-.vkappa.B blockade, and a group where constitutive expression was very low (or undetectable) and, after stimulation, expression levels strongly increased. In this group, NF-.vkappa.B blockade inhibited the viral induction of genes. This latter cluster includes chemokines, transcriptional regulators, intracellular proteins regulating translation and proteolysis, and secreted proteins (e.g., complement components, growth factor regulators). These data reveal complexity in the genetic response to NF-.vkappa.B and serve as a foundation for further informatics anal. to identify genetic features common to up- and down-regulated NF-.vkappa.B-dependent promoters.
OSC.G 59 THERE ARE 59 CAPLUS RECORDS THAT CITE THIS RECORD (59 CITINGS)
RE.CNT 92 THERE ARE 92 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 11 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:516645 CAPLUS <<LOGINID::20090921>>
DN 139:302567
TI Telomere fingerprinting for assessing chromosome number, isolate typing and recombination in the entomopathogen Beauveria bassiana
AU Padmavathi, J.; Uma Devi, K.; Rao, C. Uma Maheswara; Reddy, N. Nageswara Rao
CS Department of Botany, Andhra University, Visakhapatnam, 530 003, India
SO Mycological Research (2003), 107(5), 572-580 CODEN: MYCRER; ISSN: 0953-7562
PB Cambridge University Press
DT Journal
LA English
AB Beauveria bassiana is a popular biocontrol agent used as a 'green' pesticide in crop insect pest management. Chromosome no. has been variously reported as five, six, seven and eight in this species. The range of chromosome no. and the min. chromosome no. in this economically important fungus were assessed through telomere fingerprint anal. of a sample of 17 isolates from different and similar hosts and distant and same geog. origin. Genomic DNA digested with EcoRI, which has no cutting site in the telomere ***repeat*** sequence ***arrays*** was probed with a radioisotope-labeled (5'-TTAGGG-3')8 ***oligonucleotide*** . The probe-hybridized regions appeared as discrete bands - each representing a telomere. The no. of bands in each lane was counted and halved to arrive at the chromosome no. of that isolate. The chromosome no. varied from 5 to 10 in the different isolates. The telomere probe hybridized bands were also scored for presence or absence in a 0-1 matrix and a dendrogram based on similarities between the isolates was constructed using the NTSYS-pc ver. 2.02i software. The isolates showed very little similarity; the overall similarity was 14%. Only two isolates which were of diverse host and geog. origin showed 100% similarity. Isolates from the same epizootic that showed 43% similarity in their telomere fingerprints had 96% similarity in their RAPD (Random amplified polymorphic DNA) fingerprints with 10 primers. The genetic distances computed from any one DNA fingerprinting method thus do not reflect the true genetic similarities of the isolates. The frequency distribution pattern of the pair-wise similarities computed from telomere fingerprints hinted at the occurrence of recombination in this fungus. Telomere fingerprinting proved very useful in typing isolates since each of them was found to have a unique fingerprint. Isolates with the same chromosome no. neither showed a distinct morphol. or virulence character nor a close similarity in telomere or RAPD fingerprints to merit their subgrouping into a taxonomically relevant or practically useful unit.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 12 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:450650 CAPLUS <<LOGINID::20090921>>
DN 139:128993
TI Profiling of genes differentially expressed between fetal liver and postnatal liver using high-density oligonucleotide DNA ***array***

AU Nagata, Toshihito; Takahashi, Yasuo; Ishii, Yukimoto; Asai, Satoshi; Sugahara, Megumi; Nishida, Yayoi; Murata, Akiko; Chin, Motoaki; Schichino, Hiroyuki; Koshinaga, Tsugumichi; Fukuzawa, Masahiro; Mugishima, Hideo
CS Department of Advanced Medicine, Nihon University, Itabashi-ku, Tokyo, 173-8610, Japan
SO International Journal of Molecular Medicine (2003), 11(6), 713-721 CODEN: IJMMFG; ISSN: 1107-3756
PB International Journal of Molecular Medicine
DT Journal
LA English
AB The liver is an essential organ in humans not only for the prodn. and storage of energy but also for detoxification of chem. compds., but knowledge about changes in the gene expression profile in the human liver during the prenatal and postnatal periods is limited. Profiling of genes differentially expressed between the fetal liver (FL) and the postnatal liver (PNL) is one of the methods to investigate candidates affecting the difference in biol. characteristics between FL and PNL. To identify genes differentially expressed between FL and PNL (childhood and adult liver), we analyzed the gene expression profiles across 9 FL and 14 PNL samples using a high-d. oligonucleotide DNA ***array*** . Using Mann-Whitney U test followed by k-nearest-neighbors (supervised learning method) and hierarchical clustering (unsupervised learning method) algorithms, we found 33 genes clearly discriminating between the FL group and PNL group. The functional classification of the 33 genes identified was related to several kinds of biol. pathways, regulating the cell cycle (PCNA, CDC7L1, CCND3, YWHA1, PKMYT1), DNA replication and repair (RFC4, RECQ2, PCNA, NAP1L1), cell growth (IGF2, IGFBP2, PRSSI1), hormonal signals (AR, SRD5A1, NR113), and cellular metab. (E2-EPF, WWP1, CYP2C9, CYP2E1, CYP2A6, CYP2A7, CYP2A13, CYP4F2, CYP3A4, DDT). The results presented herein provide evidence of a differential expression profile of genes regulating the cell cycle, DNA replication and repair, cell growth, regulation of hormonal signals, and cellular metab., between FL and PNL in humans. The 33 genes identified in this study are suggested to be useful markers clearly discriminating between FL and PNL using the gene expression profile.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 13 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:215121 CAPLUS <<LOGINID::20090921>>
DN 138:181542
TI A new non-linear normalization method for reducing variability in DNA ***microarray*** experiments
AU Workman, Christopher; Jensen, Lars Juhl; Jarmer, Hanne; Berka, Randy; Gautier, Laurent; Nielsen, Henrik Bjorn; Saxild, Hans-Henrik; Nielsen, Claus; Brunak, Soren; Knudsen, Steen
CS GeneData AG, Basel, CH-4058, Switz.
SO GenomeBiology [online computer file] (2002), 3(9), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://www.genomebiology.com/content/pdf/gb-2002-3-9-research0048.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB ***Microarray*** data are subject to multiple sources of variation, of which biol. sources are of interest whereas most others are only confounding. Recent work has identified systematic sources of variation that are intensity-dependent and non-linear in nature. Systematic sources of variation are not limited to the differing properties of the cyanine dyes Cy5 and Cy3 as obsd. in cDNA ***arrays*** , but are the general case for both oligonucleotide ***microarray*** (Affymetrix GeneChips) and cDNA ***microarray*** data. Current normalization techniques are most often linear and therefore not capable of fully correcting for these effects. The authors present here a simple and robust non-linear method for normalization using ***array*** signal distribution anal. and cubic splines. These methods compared favorably to normalization using robust local-linear regression (lowess). The application off these methods to ***oligonucleotide*** ***arrays*** reduced the relative error between ***replicates*** by 5-10% compared with a std. global normalization method. Application to cDNA ***arrays*** showed improvements over the std. method and over Cy3-Cy5 normalization based on dye-swap replication. In addn., a set of known differentially regulated genes was ranked higher by the t-test. In either cDNA or Affymetrix technol., signal-dependent bias was more than ten times greater than the obsd. print-tip or spatial effects. Intensity-dependent normalization is important for both high-d. oligonucleotide ***array*** and cDNA ***array*** data. Both the regression and spline-based methods described here performed better than existing linear methods when assessed on the variability of replicate ***arrays*** . Dye-swap normalization was less effective at Cy3-Cy5 normalization than either regression or spline-based methods alone.
OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 14 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:107070 CAPLUS <<LOGINID::20090921>>
DN 138:298307
TI A variable fold-change threshold determines significance for expression ***microarrays***
AU Mariani, Thomas J.; Budhraja, Vikram; Mecham, Brigham H.; Gu, C. Charles; Watson, Mark A.; Sadovsky, Yoel
CS Division of Pulmonary and Critical Care, Department of Medicine, Brigham and Women's Hospital at Harvard Medical School, Boston, MA, 02115, USA
SO FASEB Journal (2003), 17(2), 321-323, 10.1096/fj.02-0351fje CODEN: FAJOEC; ISSN: 0892-6638
PB Federation of American Societies for Experimental Biology
DT Journal
LA English
AB The use of expression ***microarrays*** to det. bona fide changes in gene expression between exptl. paradigms is confounded by noise due to variability in measurement. To assess the variability assocd. with transcript hybridization to com. ***oligonucleotide*** -based ***microarrays*** , we generated a data set consisting of five ***replicate*** hybridizations of a single labeled cRNA target from three distinct exptl. paradigms, using the Affymetrix human U95 GeneChip set. We found that the variability of expression level in our data set is intensity-specific. We quantified the obsd. variability in our data set in order to det. significant specific. We quantified the obsd. variability in our data set in order to det. significant changes in gene expression. LOESS fitting to a plot of the std. deviation of replicates assigned a variability assocd. with a specific intensity. This allowed for the calcn. of a "variable fold-change" threshold for any abs. intensity at any level of statistical confidence. Testing of this method indicates that it removes intensity-specific bias and results in a 5- to 10-fold redn. in the no. of false-pos.

changes. We suggest that this approach can be widely used to improve prediction of significant changes in gene expression for ***oligonucleotide*** -based ***microarray*** expts. and reduce false leads, even in the absence of ***replicates*** .
OSC.G 23 THERE ARE 23 CAPLUS RECORDS THAT CITE THIS RECORD (23 CITINGS)
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 15 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:9873 CAPLUS <<LOGINID::20090921>>
DN 138:266690
TI ***Replicate*** high-density rat genome ***oligonucleotide*** ***microarrays*** reveal hundreds of regulated genes in the dorsal root ganglion after peripheral nerve injury
AU Costigan, Michael; Befort, Katia; Karchewski, Laurie; Griffin, Robert S.; D'Urso, Donatella; Allchorne, Andrew; Sitarski, Joanne; Mannion, James W.; Pratt, Richard E.; Woolf, Clifford J.
CS Department of Anesthesia and Critical Care, Massachusetts General Hospital and Harvard Medical School, Charlestown, MA, 02129, USA
SO BMC Neuroscience [online computer file] (2002), 3, No pp. given CODEN: BNMEA6; ISSN: 1471-2202 URL: http://www.biomedcentral.com/1471-2202/3/16
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: Rat oligonucleotide ***microarrays*** were used to detect changes in gene expression in the dorsal root ganglion (DRG) 3 days following sciatic nerve transection (axotomy). Two comparisons were made using two sets of triplicate ***microarrays*** , naive vs. naive and naive vs. axotomy. Results: ***Microarray*** variability was assessed using the naive vs. naive comparison. These results support use of a P < 0.05 significance threshold for detecting regulated genes, despite the large no. of hypothesis tests required. For the naive vs. axotomy comparison, a 2-fold cut off alone led to an estd. error rate of 16%; combining a > 1.5-fold expression change and P < 0.05 significance reduced the estd. error to 5%. The 2-fold cut off identified 178 genes while the combined >1.5-fold and P < 0.05 criteria generated 240 putatively regulated genes, which we have listed. Many of these have not been described as regulated in the DRG by axotomy. Northern blot, quant. slot blots and in situ hybridization verified the expression of 24 transcripts. These data showed an 83% concordance rate with the ***arrays*** ; most mismatches represent genes with low expression levels reflecting limits of ***array*** sensitivity. A significant correlation was found between actual mRNA differences and relative changes between ***microarrays*** (R2 = 0.8567). Temporal patterns of individual genes regulation varied. Conclusions: We identify parameters for ***microarray*** anal. which reduce error while identifying many putatively regulated genes. Functional classification of these genes suggest reorganization of cell structural components, activation of genes expressed by immune and inflammatory cells and down-regulation of genes involved in neurotransmission.
RE.CNT 139 THERE ARE 139 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 16 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:801722 CAPLUS <<LOGINID::20090921>>
DN 137:274122
TI Human mbt repeat-containing protein, protein and cDNA sequences, recombinant production and therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Shanghai Bode Gene Development Co., Ltd., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 35 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1333215 A 20020130 CN 2000-117027 20000707
PRAI CN 2000-117027 20000707
AB The invention relates to a human mbt repeat-contg. protein, designated as development regulation-related protein 10.45. The open reading frame of the cDNA encodes a protein with 95 amino acids, and an estd. mol. wt. of 10 kilodalton based on SDS-PAGE. The invention provides the use of polypeptide and polynucleotide in a method for treatment of various kinds of diseases, such as cancer, blood disease, HIV infection, immune diseases, growth disease, and inflammation. The invention also relates to methods, expression vectors and host cells for recombinant prodn. of said mbt repeat-contg. protein 10.45. The invention also relates to agonist and antagonist of said mbt repeat-contg. protein 10.45 and uses in therapy. The invention found that the expression profile of said mbt repeat-contg. protein 10.45 in some animal cell lines and tissues was similar to that of human mbt repeat-contg. protein.

L9 ANSWER 17 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:791946 CAPLUS <<LOGINID::20090921>>
DN 137:274053
TI Procedure and device for the replication of a high-density molecular ***array*** immobilized on a solid surface
IN Stengele, Klaus-Peter
PA Chemogenix G.m.b.H., Germany
SO Ger. Offen., 16 pp. CODEN: GWXXBX
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI DE 10116428 A1 20021017 DE 2001-10116428 20010402
PRAI DE 2001-10116428 20010402
AB A method of creating probe ***arrays*** such as DNA ***microarrays*** by replica plating of complementary sequences from a master ***array*** is described. The first high d. ***array*** is constructed by std. methods. It is then incubated with a probe library to capture and order probes from a soln. Unbound material is removed by washing at an appropriate stringency. A second surface is brought into close proximity to the first and the hybrids are eluted and transferred to the second plate to give an ***array*** that is the complement of of the master plate. The order of the ***array*** may be maintained by use of a gel or high viscosity soln. as the transfer medium. After thorough washing under strongly denaturing conditions the master plate can be reused.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 18 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:789011 CAPLUS <<LOGINID::20090921>>
DN 138:34088
TI Method of multiple parallel screening of binding specificity of biologically active compounds with nucleic acids using biochip (versions)
IN Mirzabekov, A. D.; Zasedatelev, A. S.; Krylov, A. S.; Zasedateleva, O. A.; Prokopenko, D. V.
PA Institut Molekulyarnoi Biologii im. V. A. Engel'gardta RAN, Russia
SO Russ., No pp. given CODEN: RUXXE7
DT Patent
LA Russian
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI RU 2182708 C2 20020520 RU 2000-109793 20000417
PRAI RU 2000-109793 20000417
AB The invention is relates to mol. biol., medicine, pharmacol., environment protection. An improved method of multiple parallel screening for binding specificity of biol. active compds. with double-stranded nucleic acids using biochip is presented. SUBSTANCE: biochip with immobilized oligonucleotides is prepd. and hybridization of these nucleotides with a mixt. of nonself-complementary oligonucleotides labeled with fluorescent label is carried out. Double-stranded oligonucleotides are formed on biochip that's are subjected for melting recording data and biochip is washed out. The ***repeated*** hybridization is carried out with the same mixt. of ***oligonucleotides*** labeled with fluorescent label followed by incubation of biochip with the compd. to be studied. Double-stranded oligonucleotides are melted again on biochip being these nucleotides are in complex with biol. active compd. to be studied. Data are recorded and m.ps. of double-stranded oligonucleotides are detd. in the presence and absence of compd. to be studied and difference of m.p. is measured. Based on total data obtained the specificity of binding of compd. to be studied is detd. The universal biochip where in its units all possible hexanucleotides are immobilized is used preferably. Fluorescent dye can be Texas Red. Oligonucleotides are melted using a thermotable. The mass of exptl. data is treated using the computer program preferably. Dye Hoechst 33258 or protein HU can be used as compd. to be studied. By the second variant method involves incubation of biochip with fluorescent compd. to be studied immediately after prepg. biochip with oligonucleotides immobilized on its. Method ensures to carry out the comparative exptl. anal. of relationship degree of chem. compd. to all possible sequences of nucleic acid in the range of binding site.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L9 ANSWER 19 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:757296 CAPLUS <<LOGINID::20090921>>
DN 137:243127
TI Human tetrapeptide repeats containing protein 15 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1331124 A 20020116 CN 2000-116728 20000626
PRAI CN 2000-116728 20000626
AB The invention provides cDNA sequences of a novel human tetrapeptide repeats contg. protein 15 cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. The invention further relates to applications of related gene or protein products for the treatment of related diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L9 ANSWER 20 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:706469 CAPLUS <<LOGINID::20090921>>
DN 137:196658
TI Protein and cDNA sequences of human DNA CGG repeat-binding protein 16.17 and therapeutical uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1326990 A 20011219 CN 2000-116383 20000607 WO 2002026812 A1 20020404 WO 2001-CN910 20010604 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2001089517 A 20020408 AU 2001-89517 20010604
PRAI CN 2000-116383 A 20000607 WO 2001-CN910 W 20010604
AB The invention provides the protein and cDNA sequences of a novel human DNA CGG repeat-binding protein 16.17 with the mol. wt. of 16 kilodaltons cloned from human fetal brain. In particular, the invention discloses that the gene encoding this protein has a similar gene expression pattern with gene encoding DNA CGG repeat-binding protein. The invention also relates to construction of DNA CGG repeat-binding protein 16.17 expression vector for prepn. of recombinant protein using prokaryotes or eukaryotes. The invention relates to prepn. of antibody against this protein. The invention further relates to the PCR primers, nucleic acid probes, DNA fragments and protein agonists or antagonists specific for this gene or gene product for the diagnosis as well as treatment of various diseases, such as

neurodegenerative diseases, growth and development disorders, etc.

L9 ANSWER 21 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:697440 CAPLUS <<LOGINID::20090921>>
DN 138:803
TI Comparing three methods for variance estimation with ***duplicated*** high density ***oligonucleotide*** ***arrays***
AU Huang, Xiaohong; Pan, Wei
CS Division of Biostatistics, School of Public Health, University of Minnesota, Minneapolis, MN, 55455-0378, USA
SO Functional & Integrative Genomics (2002), 2(3), 126-133
CODEN: FIGUBY; ISSN: 1438-793X
PB Springer-Verlag
DT Journal
LA English
AB ***Microarray*** expts. are being increasingly used in mol. biol. A common task is to detect genes with differential expression across two exptl. conditions, such as two different tissues or the same tissue at two time points of biol. development. To take proper account of statistical variability, some statistical approaches based on the t-statistic have been proposed. In constructing the t-statistic, one needs to est. the variance of gene expression levels. With a small no. of replicated ***array*** expts., the variance estn. can be challenging. For instance, although the sample variance is unbiased, it may have large variability, leading to a large mean squared error. For duplicated ***array*** expts., a new approach based on simple averaging has recently been proposed in the literature. Here we consider two more general approaches based on nonparametric smoothing. Our goal is to assess the performance of each method empirically. The three methods are applied to a colon cancer data set contg. 2,000 genes. Using two ***arrays*** , we compare the variance ests. obtained from the three methods. We also consider their impact on the t-statistics. Our results indicate that the three methods give variance ests. close to each other. Due to its simplicity and generality, we recommend the use of the smoothed sample variance for data with a small no. of replicates.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 22 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:696540 CAPLUS <<LOGINID::20090921>>
DN 137:212846
TI Fluorescence assay for DNA modifying enzymes
IN Reich, Norbert Otto; Allan, Barrett W.; Lindstrom, William Maxwell; Putzke, Aaron Paul
PA Regents of the University of California, USA
SO U.S. Pat. Appl. Publ., 6 pp. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 20020127593 A1 20020912 US 2002-94364 20020308 WO 2002072891 A1 20020919 WO 2002-US7413 20020311 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002255701 A1 20020924 AU 2002-255701 20020311
PRAI US 2001-276875P P 20010312 US 2002-94364 A 20020308 WO 2002-US7413 W 20020311
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB A method of assaying compds. for their ability to effect enzymes including enhancing or inhibiting the effect of those enzymes on double stranded DNA sequences is disclosed. The method comprises providing a modified nucleotide sequence comprised of a base analog which analog is characterized by increased fluorescence when moved out of its normal helical position, the sequence having a complimentary sequence hybridized thereto to provide a double stranded sequence. The modified sequence contg. the base analog is brought into contact with the enzyme which enzyme is characterized by effecting the 3-dimensional position of the analog within the sequence. The enzyme is brought into contact with the sequences in the presence of a compd. being assayed. By knowing the amt. of increased fluorescence the enzyme would normally have on the sequence is possible to det. the inhibitory or enhancing effect of the compd. on the enzyme.

L9 ANSWER 23 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:696530 CAPLUS <<LOGINID::20090921>>
DN 137:227598
TI Replica amplification of nucleic acid ***arrays***
IN Church, George M.; Mitra, Rob
PA USA
SO U.S. Pat. Appl. Publ., 33 pp., Cont.-in-part of U.S. Ser. No. 267,496. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 7 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 20020127552 A1 20020912 US 2000-573465 20000517 US 6432360 B1 20020813 US 1998-143014 19980828 US 6485944 B1 20021126 US 1999-267496 19990312 AU 2002301870 A1 20030313 AU 2002-301870 20021107
PRAI US 1997-61511P P 19971010 US 1998-76570P P 19980302 US 1998-143014 B2 19980828 US 1999-267496 A2 19990312 AU 2000-38761 A3 20000310
AB Disclosed are improved methods of making and using immobilized ***arrays*** of nucleic acids, particularly methods for producing replicas of such ***arrays*** . Included are methods for producing high d. ***arrays*** of nucleic acids and replicas of such ***arrays*** , as well as methods for preserving the resoln. of ***arrays*** through rounds of replication. A master ***array*** is prepd. and the immobilized sequences are amplified by primer extension. The extension takes place with a second immobilizing surface very close to the master ***array*** (within the radius of a hemisphere swept out by the immobilized oligonucleotide.). As the primer extension products are liberated from the hybrid, e.g. by thermal denaturation, they are captured by the immobilizing surface. The extension product may include reactive groups, esp. at the 3'-end to increase the efficiency of immobilization. Also included are methods which take advantage of the

availability of replicas of ***arrays*** for increased sensitivity in detection of sequences on ***arrays*** . Improved methods of sequencing nucleic acids immobilized on ***arrays*** utilizing single copies of ***arrays*** and methods taking further advantage of the availability of replicas of ***arrays*** are disclosed. The improvements lead to higher fidelity and longer read lengths of sequences immobilized on ***arrays*** . Methods are also disclosed which improve the efficiency of multiplex PCR using ***arrays*** of immobilized nucleic acids.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L9 ANSWER 24 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:620397 CAPLUS <<LOGINID::20090921>>
DN 137:136120
TI Human replication initiation recognition complex subunit ORC413.64 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1327995 A 20011226 CN 2000-116447 20000612
PRAI CN 2000-116447 20000612
AB The invention provides cDNA sequences of a novel human replication initiation recognition complex subunit ORC413.64 (also called ORC413.64) cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. The invention further relates to applications of related gene or protein products for the treatment of related diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L9 ANSWER 25 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:615306 CAPLUS <<LOGINID::20090921>>
TI Model studies of oligonucleotide immobilization on silica surfaces
AU Horgan, Adrian; Jin, Lei; Levicky, Rastislav
CS Department of Chemical Engineering, Columbia University, New York, NY, 10027, USA
SO Abstracts of Papers, 224th ACS National Meeting, Boston, MA, United States, August 18-22, 2002 (2002), COLL-318 Publisher: American Chemical Society, Washington, D. C. CODEN: 69CZPZ
DT Conference; Meeting Abstract
LA English
AB DNA has been immobilized on many different surfaces using various chemistries for use in genetic diagnostics e.g. DNA ***microarrays*** . A covalent attachment strategy is generally regarded as the best way to immobilize oligonucleotides on glass surfaces. The most common method of linking glass and DNA covalently is to modify the glass surface in a pre-treatment step with a silane. The silylated surface is then modified using a heterobifunctional crosslinker possessing two dissimilar functionalities with different chem. specificities, one of which is selective for the silane. The oligonucleotide is then tethered to the support through reaction with the free end of the immobilized crosslinker. Due to sensitivity issues, it is often difficult to closely characterize each chem. step in the sequence of reactions used to immobilize the nucleic acid. Yet, it is extremely important as any exptl. variation will affect film quality and stability, which in turn will affect reliability and ***repeatability*** and the levels of ***oligonucleotide*** probe immobilization and target hybridization. In this talk, detailed characterization of common immobilization methods will be presented, based on the study of high surface area solid supports.

L9 ANSWER 26 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:573241 CAPLUS <<LOGINID::20090921>>
DN 137:137208
TI Diagnosis kit for trisomy 13 including oligonucleotides
IN Waschuetza, Stefanie; Wehmeier, Lutz
PA Adnagen A.-G., Germany
SO Ger. Offen., 8 pp. CODEN: GWXXBX
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI DE 10102687 A1 20020801 DE 2001-10102687 20010122
PRAI DE 2001-10102687 20010122
AB The invention concerns a test kit for the prenatal diagnosis of trisomy 13 from maternal blood or amniotic fluid that includes at least two pairs of ***oligonucleotides*** that are primers for a PCR to amplify regions of short tandem ***repeat*** (STR) DNA from human chromosome 13. Preferably three pairs of primers are used; they are immobilized as DNA ***arrays*** ; the primers can be fluorescent labeled for detection. The test kit further contains the reagents for the PCR.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L9 ANSWER 27 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:555682 CAPLUS <<LOGINID::20090921>>
DN 137:104752
TI Probes to repeat sequence-free genomic regions for use in high throughput screening of genomes
IN Collins, Colin; Volik, Stanislav V.; Gray, Joe W.; Albertson, Donna G.; Pinkel, Daniel
PA The Regents of the University of California, USA
SO PCT Int. Appl., 30 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002057481 A2 20020725 WO 2002-US365 20020107 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 20030022166 A1 20030130 US 2001-766450

20010119 AU 2002245225 A1 20020730 AU 2002-245225 20020107
PRAI US 2001-766450 A 20010119 WO 2002-US365 W 20020107
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention provides a rapid, efficient, and automated method for identifying unique sequences within the genome. This invention involves the identification of repeat sequence-free subregions within a genomic region of interest as well as the detn. of which of those repeat sequence-free subregions are truly unique within the genome. Once the truly unique subregions are identified, primer sequences are generated that are suitable for the amplification of sequences, e.g., for use as probes or ***array*** targets, within the unique subregions.

L9 ANSWER 28 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:538043 CAPLUS <<LOGINID::20090921>>
DN 137:89426
TI Method and kit for prenatal diagnosis of fetal chromosome 21 trisomy
IN Waschuetza, Stefanie; Tamak, Cengiz; Wehmeier, Lutz
PA Adnagen A.-G., Germany
SO Ger. Offen., 10 pp. CODEN: GWXXBX
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI DE 10059776 A1 20020718 DE 2000-10059776 20001201
PRAI DE 2000-10059776 20001201
AB The invention concerns a method and kit for prenatal diagnosis of human fetus chromosome 21 trisomy by anal. of maternal blood or amniotic fluid. The diagnostic kit contains at least two pairs of ***oligonucleotides*** (reverse and forward primers), that are suitible to be used as PCR primers, one for each of the two complementary strands of the short tandem ***repeat*** DNA region of human chromosome 21.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 29 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:516233 CAPLUS <<LOGINID::20090921>>
DN 137:42575
TI Method for a flexible production of oligomer ***arrays***
IN Berlin, Kurt
PA Epigenomics Ag, Germany
SO Ger. Offen., 8 pp. CODEN: GWXXBX
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI DE 10065815 A1 20020711 DE 2000-10065815 20001222
PRAI DE 2000-10065815 20001222
AB The invention concerns a device for a flexible prodn. of immobilized oligomer ***arrays*** that can be used for detecting genetic polymorphism and diagnosis of diseases. In the first step the oligomers are synthesized by placing the monomer on the surface by the aid of needles, whereby it reacts with the immobilized oligomer, that does not contain a protective group at its termini. The core of the device is an ***array*** of needles which cannot move and an ***array*** of receptacles for the monomers, whereby the receptacles can slide past one another. In the second step the monomer is modified by an acid-labile protective group by applying a non-volatile, acidic reagent to the fixed phase in a form of one or several drops. In the third step on the same place of the surface, at which the acidic reagent was applied, a buffer is added for neutralization and removal of the reagents and buffer in a wash step. The steps are ***repeated*** , until ***oligonucleotides*** of the desired sequence and length are produced.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 30 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:359258 CAPLUS <<LOGINID::20090921>>
DN 137:320900
TI Empirical characterization of the expression ratio noise structure in high-density oligonucleotide ***arrays***
AU Naef, Felix; Hacker, Coleen R.; Patil, Nila; Magnasco, Marcelo
CS Mathematical Physics Laboratory, Center for Studies in Physics and Biology, The Rockefeller University, New York, NY, 10021, USA
SO GenomeBiology [online computer file] (2002), 3(4), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebiology.com/2002/3/4/research/0018/
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB High-d. oligonucleotide ***arrays*** (HDONAs) are a powerful tool for assessing differential mRNA expression levels. To establish the statistical significance of an obsd. change in expression, one must take into account the noise introduced by the enzymic and hybridization steps, called type I noise. We undertake an empirical characterization of the exptl. repeatability of results by carrying out statistical anal. of a large no. of duplicate HDONA expts. We assign scoring functions for expression ratios and assocd. quality measures. Both the perfect-match (PM) probes and the differentials between PM and single-mismatch (MM) probes are considered as raw intensities. We then calc. the log-ratio of the noise structure using robust ests. of their intensity-dependent variance. The noise structure in the log-ratios follows a local log-normal distribution in both the PM and PM-MM cases. Significance relative to the type I noise can therefore be quantified reliably using the local std. deviation (SD). We discuss the intensity dependence of the SD and show that ratio scores greater than 1.25 are significant in the mid- to high-intensity range. The noise inherent in HDONAs is characteristically dependent on intensity and can be well described in terms of local normalization of log-ratio distributions. Therefore, robust ests. of the local SD of these distributions provide a simple and powerful way to assess significance (relative to type I noise) in differential gene expression, and will be helpful in practice for improving the reliability of predictions from hybridization expts.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 31 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2002:339132 CAPLUS <<LOGINID::20090921>>
DN 137:211420
TI Stem-loop oligonucleotides: a robust tool for molecular biology and biotechnology
AU Broude, Natalia E.
CS Center for Advanced Biotechnology and Dept of Biomedical Engineering, Boston University, Boston, MA, 02215, USA
SO Trends in Biotechnology (2002), 20(6), 249-256 CODEN: TRBIDM; ISSN: 0167-7799
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review. The specific structural features of stem-loop (hairpin) DNA constructs provide increased specificity of target recognition. Recently, several robust assays have been developed that exploit the potential of structurally constrained oligonucleotides to hybridize with their cognate targets. Here, this paper reviews new diagnostic approaches based on the formation of stem-loop DNA oligonucleotides: mol. beacon methodol., suppression PCR approaches and the use of hairpin probes in DNA ***microarrays*** . The advantages of these techniques over existing ones for sequence-specific DNA detection, amplification and manipulation are discussed.
OSC.G 83 THERE ARE 83 CAPLUS RECORDS THAT CITE THIS RECORD (83 CITINGS)
RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 32 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:318006 CAPLUS <<LOGINID::20090921>>
DN 137:137044
TI An assessment of Motorola CodeLink ***microarray*** performance for gene expression profiling applications
AU Ramakrishnanm, Ramesh; Dorris, David; Lublinsky, Anna; Nguyen, Allen; Domanus, Marc; Prokhorova, Anna; Gieser, Linn; Touma, Edward; Lockner, Randall; Tata, Murthy; Zhu, Xiaomei; Patterson, Marcus; Shippy, Richard; Sendera, Timothy J.; Mazumder, Abhijit
CS Motorola Life Sciences, Northbrook, IL, 60062, USA
SO Nucleic Acids Research (2002), 30(7), e30/1-e30/12 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB DNA ***microarrays*** enable users to obtain information on differences in transcript abundance on a massively parallel scale. Recently, however, data analyses have revealed potential pitfalls related to image acquisition, variability and misclassifications in replicate measurements, cross-hybridization and sensitivity limitations. We have generated a series of anal. tools to address the manufg., detection and data anal. components of a ***microarray*** expt. Together, we have used these tools to optimize performance in an expression profiling study. We demonstrate three significant advantages of the Motorola CodeLink platform: sensitivity of one copy per cell, coeffs. of variation of 10% in the hybridization signals across slides and across target prepns., and specificity in distinguishing highly homologous sequences. Slides where ***oligonucleotide*** probes are spotted in 6-fold redundancy were used to demonstrate the effect of ***replication*** on data quality. Lastly, the differential expression ratios obtained with the CodeLink expression platform were validated against those obtained with quant. reverse transcription-PCR assays for 54 genes.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 33 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:214668 CAPLUS <<LOGINID::20090921>>
DN 137:150359
TI Identification of genes regulated by dexamethasone in multiple myeloma cells using oligonucleotide ***arrays***
AU Chauhan, Dharminder; Auclair, Daniel; Robinson, Elisabeth K.; Hideshima, Teru; Li, Guilan; Podar, Klaus; Gupta, Deepak; Richardson, Paul; Schlossman, Robert L.; Krett, Nancy; Chen, Lan Bo; Munshi, Nikhil C.; Anderson, Kenneth C.
CS The Jerome Lipper Multiple Myeloma Center, Department of Adult Oncology, Dana Farber Cancer Institute, Harvard Medical School, Boston, MA, 02115, USA
SO Oncogene (2002), 21(9), 1346-1358 CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English
AB Our previous studies have characterized Dexamethasone (Dex)-induced apoptotic signaling pathways in multiple myeloma (MM) cells; however, related transcriptional events are not fully defined. In the present study, gene expression profiles of Dex-treated MM cells were detd. using oligonucleotide ***arrays*** . Dex triggers early transient induction of many genes involved in cell defense/repair-machinery. This is followed by induction of genes known to mediate cell death and repression of growth/survival-related genes. The mol. and genetic alterations assocd. with Dex resistance in MM cells are also unknown. We compared the gene expression profiles of Dex-sensitive and Dex-resistant MM cells and identified a no. of genes which may confer Dex-resistance. Finally, gene profiling of freshly isolated MM patient cells validates our in vitro MM cell line data, confirming an in vivo relevance of these studies. Collectively, these findings provide insights into the basic mechanisms of Dex activity against MM, as well as mechanisms of Dex-resistance in MM cells. These studies may therefore allow improved therapeutic uses of Dex, based upon targeting genes that regulate MM cell growth and survival.
OSC.G 79 THERE ARE 79 CAPLUS RECORDS THAT CITE THIS RECORD (79 CITINGS)
RE.CNT 67 THERE ARE 67 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 34 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:194380 CAPLUS <<LOGINID::20090921>>
DN 136:211889
TI A human 24 kilodalton leucine-repeat motif-containing protein, protein and cDNA sequences, recombinant production and therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Bodao Gene Tech. Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 33 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1306991 A 20010808 CN 2000-111592 20000128

PRAI CN 2000-111592 20000128
AB The invention relates to a human leucine-repeat motif-contg. protein. The open reading frame of the cDNA encodes a protein with 218 amino acids, and an estd. mol. wt. of 24 kilodalton based on SDS-PAGE. The invention provides the use of polypeptide and polynucleotide in a method for treatment of various kinds of diseases, such as cancer, blood disease, HIV infection, immune diseases, and inflammation. The invention also relates to methods, expression vectors and host cells for recombinant prodn. of said leucine-repeat motif-contg. protein. The invention also relates to agonist and antagonist of said leucine-repeat motif-contg. protein and uses in therapy. The expression of said leucine-repeat motif-contg. protein in pharynx cancer tissue is significantly different from that in normal pharynx tissue.

L9 ANSWER 35 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:183823 CAPLUS <<LOGINID::20090921>>
DN 136:227907
TI Calibration of nucleic acid ***array*** data employing calibrating oligonucleotide probes
IN Wobler, Paul K.; Delenstarr, Glenda C.
PA Agilent Technologies, Inc., USA
SO Eur. Pat. Appl., 32 pp. CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI EP 1186673 A2 20020313 EP 2001-307665 20010910 EP 1186673 A3 20030326 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
PRAI US 2000-659173 A 20000911
AB A method for calibrating different types of signals scanned from a mol. ***array*** , or calibrating signals scanned from different mol. ***arrays*** , by employing calibrating probes that generate signals proportional to the total concns. of labeled target mols. to which the mol. ***array*** probes are directed over an entire range of sample solns., and mol. ***arrays*** incorporating sets of calibrating probes. For mol. ***arrays*** that include oligonucleotide probes directed to cDNA targets produced by reverse transcription of mRNA mols., suitable probes for calibrating features include: (1) poly(A) ***oligonucleotides*** of varying lengths; (2) ***oligonucleotides*** having sequences complementary to cDNA copies of cDNA transcripts of Alu ***repeat*** sequences in human mRNA mols.; (3) ***oligonucleotide*** probes complementary to arbitrary synthetic sequences incorporated into 5'-end primers used to initiate reverse transcription of mRNA mols.; and (4) random ***oligonucleotide*** probes of varying lengths with high probability of being complementary to relatively large fractions of target mols. Exptl. verification employing poly(A) oligonucleotide probes was obtained using purified mRNA from human K-562 cells with Cy3 and Cy5 fluorescent labels. The linear relationship between log(signalCy5) and log(signalCy3) for the general gene-specific probes coincides quite well with the ratios for the normalization probes.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 36 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:143237 CAPLUS <<LOGINID::20090921>>
DN 136:178960
TI Using the specific interactions between nucleic acids to create complementary copies of ***arrays*** of oligonucleotides
IN Furste, Jens Peter; Klussmann, Sven; Klein, Thomas; Von Kiedrowski, Gunter
PA Noxxon Pharma AG, Germany
SO U.S. Pat. Appl. Publ., 33 pp., Cont.-in-part of Appl. No. PCT/DE99/03856. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI US 20020022275 A1 20020221 US 2001-866513 20010525 US 6534271 B2 20030318 DE 19854946 A1 20000608 DE 1998-19854946 19981127 DE 19854946 C2 20020103 WO 2000032809 A2 20000608 WO 1999-DE3856 19991126 WO 2000032809 A3 20001019 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI DE 1998-19854946 A 19981127 WO 1999-DE3856 A2 19991126
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The invention relates to a method for cloning and copying genetic material on surfaces as well as copying biol. material insofar as it, in a broader sense, can be classified in a ligand receptor system. The invention thus relates, in particular, to a method for propagating ligands and receptors on at least two surfaces which comprises one or several of the following cycles: immobilizing a ligand on a first surface of a solid phase; adding a soln. of receptors and binding complementary receptors to the ligands; transferring the receptor to an addnl. surface and immobilizing the receptor at that location; attaching an addnl. ligand to the immobilized receptor; transferring the ligand to a surface and immobilizing the same at that location. Nucleic acids are also understood as a ligand/receptor system.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L9 ANSWER 37 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:94044 CAPLUS <<LOGINID::20090921>>
DN 137:42226
TI Characterization of Variability in Large-Scale Gene Expression Data: Implications for Study Design
AU Novak, Jaroslav P.; Sladek, Robert; Hudson, Thomas J.
CS Montreal Genome Centre, McGill University Health Centre, Montreal, QC, H3G 1A4, Can.
SO Genomics (2002), 79(1), 104-113 CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
AB Large-scale gene expression measurement techniques provide a unique opportunity to gain insight into biol. processes under normal and pathol. conditions. To interpret the changes in expression profiles for thousands of genes, we face the nontrivial

problem of understanding the significance of these changes. In practice, the sources of background variability in expression data can be divided into three categories: tech., physiol., and sampling. To assess the relative importance of these sources of background variation, we generated ***replicate*** gene expression profiles on high-d. Affymetrix GeneChip ***oligonucleotide*** ***arrays*** , using either identical RNA samples or RNA samples obtained under similar biol. states. We derived a novel measure of dispersion in two-way comparisons, using a linear characteristic function. When comparing expression profiles from replicate tests using the same RNA sample (a test for tech. variability), we obsd. a level of dispersion similar to the pattern obtained with RNA samples from replicate cultures of the same cell line (a test for physiol. variability). On the other hand, a higher level of dispersion was obsd. when tissue samples of different animals were compared (an example of sampling variability). This implies that, in expts. in which samples from different subjects are used, the variation induced by the stimulus may be masked by non-stimuli-related differences in the subjects' biol. state. These analyses underscore the need for replica expts. to reliably interpret large-scale expression data sets, even with simple ***microarray*** expts. (c) 2002 Academic Press.
OSC.G 108 THERE ARE 108 CAPLUS RECORDS THAT CITE THIS RECORD (108 CITINGS)
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 38 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:845467 CAPLUS <<LOGINID::20090921>>
DN 136:81444
TI Characterization of the stability and folding of H2A.Z chromatin particles: Implications for transcriptional activation
AU Abbott, D. Wade; Ivanova, Vessela S.; Wang, Xiaoying; Bonner, William M.; Ausio, Juan
CS Department of Biochemistry and Microbiology, University of Victoria, Victoria, BC, V8W 3P6, Can.
SO Journal of Biological Chemistry (2001), 276(45), 41945-41949 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB H2A.Z and H2A.1 nucleosome core particles and oligonucleosome ***arrays*** were obtained using recombinant versions of these histones and a native histone H2B/H3/H4 complement reconstituted onto appropriate DNA templates. Anal. of the reconstituted nucleosome core particles using native polyacrylamide gel electrophoresis and DNase I footprinting showed that H2A.Z nucleosome core particles were almost structurally indistinguishable from its H2A.1 or native chicken erythrocyte counterparts. While this result is in good agreement with the recently published crystallog. structure of the H2A.Z nucleosome core particle, the ionic strength dependence of the sedimentation coeff. of these particles exhibits a substantial destabilization, which is most likely the result of the histone H2A.Z-H2B dimer binding less tightly to the nucleosome. Anal. ultracentrifuge anal. of the H2A.Z 208-12, a DNA template consisting of 12 tandem ***repeats*** of a 208-base pair sequence derived from the sea urchin Lytechinus variegatus 5 S rRNA gene, reconstituted ***oligonucleosome*** complexes in the absence of histone H1 shows that their NaCl-dependent folding ability is significantly reduced. These results support the notion that the histone H2A.Z variant may play a chromatin-destabilizing role, which may be important for transcriptional activation.
OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)
RE.CNT 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 39 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:798387 CAPLUS <<LOGINID::20090921>>
DN 135:353801
TI A human 49 kilodalton subunit of replication factor C-like protein, protein and cDNA sequences, tissue distribution, recombinant production and therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Biowindow Gene Development Inc. Shanghai, Peop. Rep. China
SO PCT Int. Appl., 34 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001081537 A2 20011101 WO 2001-CN598 20010423
WO 2001081537 A3 20020228
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
CN 1320625 A 20011107 CN 2000-115468 20000427
AU 2001070437 A 20011107 AU 2001-70437 20010423
PRAI CN 2000-115468 A 20000427
WO 2001-CN598 W 20010423
AB The invention relates to a subunit of replication factor C-like protein from human. The open reading frame of the cDNA encodes a protein with 441 amino acids, and an estd. mol. wt. of 49 kilodalton based on SDS-PAGE. The invention provides the use of polypeptide and polynucleotide in a method for treatment of various kinds of diseases, such as cancer, blood disease, growth disorders, HIV infection, immune diseases and inflammation. The invention also relates to methods, expression vectors and host cells for recombinant prodn. of said replication factor C-like protein subunit. The invention also relates to agonist and antagonist of said replication factor C-like protein subunit and uses in therapy. The tissue expression profile of said replication factor C-like protein subunit is similar to that of human replication factor C 37 kilodalton subunit.

L9 ANSWER 40 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:792255 CAPLUS <<LOGINID::20090921>>
DN 135:328915
TI Method and apparatus for fabricating replicate ***arrays*** of nucleic acid molecules
IN Schleifer, Arthur; Caren, Michael P.; Leonard, Leslie A.; Hotz, Charles Z.; Perbost, Michel G. M.
PA Agilent Technologies, Inc., USA
SO U.S., 16 pp. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE

PI US 6309828 B1 20011030 US 1998-195421 19981118
PRAI US 1998-195421 19981118
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB A method and app. for fabricating replicate ***arrays*** of nucleic acid mols. include the prepn. of the mols. and the application of the mols. onto a substrate in an ordered ***array*** . The app. comprises a synthesis unit and a plurality of outlets. The synthesis unit comprises a plurality of synthesis chambers that are spatially arranged relative to each other to provide an ***array*** suitable for conducting parallel nucleic acid syntheses. The chambers are suitable for contg. discrete compns. of nucleic acid mols. Each outlet of the plurality of outlets communicates with a single synthesis chamber. The plurality of outlets are configured such that nucleic acid mols. can be removed from the chambers through the outlet and deposited onto the substrate in an ordered ***array*** that corresponds to the spatial arrangement of the synthesis chambers.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 41 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:763239 CAPLUS <<LOGINID::20090921>>
DN 135:314403
TI Diagnosis of diseases associated with DNA replication using oligomer probes to detect cytosine methylation state
IN Olek, Alexander; Piepenbrock, Christian; Berlin, Kurt
PA Epigenomics A.-G., Germany
SO PCT Int. Appl., 23 pp. CODEN: PIXXD2
DT Patent
LA English PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001077377 A2 20011018 WO 2001-EP3971 20010406 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR
PRAI DE 2000-10019058 20000406 DE 2000-10019173 20000407 DE 2000-10032529 20000630 DE 2000-10043826 20000901
AB The present invention is based on the discovery that cytosine methylations patterns in genomic DNA are particularly suitable for diagnosis and/or therapy of diseases assocd. with DNA replication. Thus, the chem. modified genomic sequences of genes assocd. with DNA ***replication*** , and ***oligonucleotides*** and/or peptide nucleic acid oligomers for detecting the cytosine methylation state of DNA ***replication*** genes are provided. Specific reaction of bisulfite and subsequent alk. hydrolysis converts cytosine to uracil, which corresponds to thymidine in its base pairing behavior. However, 5-methylcytosine remains unmodified under these conditions. Consequently, the original DNA is converted in such a manner that methylcytosine, which originally could not be distinguished from cytosine by its hybridization behavior, can now be detected as the only remaining cytosine using "normal" mol. biol. techniques. The oligomer probes according to the present invention, contg. at least one CpG dinucleotide, constitute important and effective tools which make it possible to ascertain the genetic and epigenetic parameters of genes assocd. with DNA replication. The invention is exemplified by methylation anal. of gene MLH1.

L9 ANSWER 42 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:758141 CAPLUS <<LOGINID::20090921>>
DN 136:257893
TI Replication dynamics of the yeast genome
AU Raghuraman, M. K.; Winzeler, Elizabeth A.; Collingwood, David; Hunt, Sonia; Wodicka, Lisa; Conway, Andrew; Lockhart, David J.; Davis, Ronald W.; Brewer, Bonita J.; Fangman, Walton L.
CS Department of Genetics, University of Washington, Seattle, WA, 98195, USA
SO Science (Washington, DC, United States) (2001), 294(5540), 115-121 CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English
AB ***Oligonucleotide*** ***microarrays*** were used to map the detailed topog. of chromosome ***replication*** in the budding yeast Saccharomyces cerevisiae. The times of replication of thousands of sites across the genome were detd. by hybridizing replicated and unreplicated DNAs, isolated at different times in S phase, to the ***microarrays*** . Origin activations take place continuously throughout S phase but with most firings near mid-S phase. Rates of replication fork movement vary greatly from region to region in the genome. The two ends of each of the 16 chromosomes are highly correlated in their times of replication. This ***microarray*** approach is readily applicable to other organisms, including humans.
OSC.G 285 THERE ARE 285 CAPLUS RECORDS THAT CITE THIS RECORD (285 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 43 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:712142 CAPLUS <<LOGINID::20090921>>
DN 136:35557
TI Distinctive molecular profiles of high-grade and low-grade gliomas based on oligonucleotide ***microarray*** analysis
AU Rickman, David S.; Bobek, Miroslav P.; Misek, David E.; Kuick, Rork; Blaivas, Mila; Kurnit, David M.; Taylor, Jeremy; Hanash, Samir M.
CS Departments of Pediatrics, University of Michigan Medical School, Ann Arbor, MI, 48109, USA
SO Cancer Research (2001), 61(18), 6885-6891 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Astrocytomas are heterogeneous intracranial glial neoplasms ranging from the highly aggressive malignant glioblastoma multiforme (GBM) to the indolent, low-grade pilocytic astrocytoma. We have investigated whether DNA ***microarrays*** can identify gene expression differences between high-grade and low-grade glial tumors. We compared the transcriptional profile of 45 astrocytic tumors including 21 GBMs and 19 pilocytic astrocytomas using oligonucleotide-based ***microarrays*** . Of the .apprx.6800 genes that were analyzed, a set of 360 genes provided a mol. signature that

distinguished between GBMs and pilocytic astrocytomas. Many transcripts that were increased in GBM were not previously assocd. with gliomas and were found to encode proteins with properties that suggest their involvement in cell proliferation or cell migration. ***Microarray*** -based data for a subset of genes was validated using real-time quant. reverse transcription-PCR. Immunohistochem. anal. also localized the protein products of specific genes of interest to the neoplastic cells of high-grade astrocytomas. Our study has identified a large no. of novel genes with distinct expression patterns in high-grade and low-grade gliomas.
OSC.G 151 THERE ARE 151 CAPLUS RECORDS THAT CITE THIS RECORD (151 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 44 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:566885 CAPLUS <<LOGINID::20090921>>
DN 135:153076
TI C-3' protected nucleotides for oligonucleotides immobilization and solid-phase synthesis
IN Huang, Yih; Huang, Tai-nang; Shen, Ming
PA Linden Technologies, Inc., USA
SO PCT Int. Appl., 53 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001055451 A1 20010802 WO 2001-US2689 20010126 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 20010044530 A1 20011122 US 2001-770886 20010126 US 6489466 B2 20021203 US 20030009027 A1 20030109 US 2002-191087 20020709 US 20030013868 A1 20030116 US 2002-191122 20020709
PRAI US 2000-178720P P 20000128 US 2000-189804P P 20000316 US 2001-770886 A3 20010126
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
OS CASREACT 135:153076
AB In one aspect, this invention is directed to a method of producing an immobilized oligonucleotide on a substrate to which a first nucleotide is covalently attached via its C-5' oxygen. The first nucleotide can be a nucleotide monomer or the 5' terminal nucleotide of a nucleotide polymer. In general, such a first nucleotide includes a modified nucleotide tethered to a support substrate through a linking group. In particular, the modified nucleotide is constructed such that the C-5' end of the nucleotide is tetherable to the linking group and the C-3' end is available for further controlled modification, e.g., addn. of other nucleotides in specific sequences to the immobilized nucleotide. Addnl., the linking group is of sufficient length to allow the immobilized nucleotide to be used to synthesize and screen ***arrays*** of nucleotide oligomers, e.g., enzymic C-3' primer extension. In another aspect, the invention provides a method for in situ solid phase oligonucleotide synthesis with C-5' attached to the substrate, thereby producing oligonucleotides which are a polymer of nucleotides. The method covers an in situ deprotection-activation-coupling cycle of oligonucleotide synthesis that includes covalently coupling a modified nucleotide via its C-5' oxygen to an immobilized hydroxy, wherein the modified nucleotide includes a C-3' photolabile protecting group and a C-5' hydroxy group, and also wherein the immobilized hydroxy group is activated with a phosphorous activating group. The synthesis includes sequentially deprotecting photolabile group from the C-3' oxygen of an immobilized nucleotide at terminus, activating the C-3' oxygen at terminus, in situ, with an activating phosphorous group, and coupling C-3' protected nucleotides to the activated nucleotide at terminus. Optionally, the cycles of deprotecting, activating, and coupling can be ***repeated*** until a desired ***oligonucleotide*** is obtained. Typically, the immobilized C-3' oxygen is activated with a phosphorous group such as a phosphoramidite, [(i-Pr)2 N]POCH2CH2CN. The produced oligonucleotide can be further involved in enzyme-catalyzed reactions, e.g., polymerase mediated primer extension. The C-3' hydroxy group on the immobilized nucleotide at terminus can be activated again in-situ to form phosphoramidite for coupling the next non-immobilized nucleotide or oligonucleotide having a C-5' hydroxy group. Alternatively, the C-3' hydroxy group on the immobilized nucleotide can couple with a non-immobilized nucleotide or oligonucleotide having an C-5' activated group and a C-3' photolabile protecting group. The invention provides one or more of the following advantages. The in situ deprotection-activation-coupling oligonucleotide synthesis is economical and versatile and generates solid phase phosphoramidite that exhibits unexpected high efficiency in coupling with sequentially added C-3' photolabile group protected nucleotides. Addnl., excess C-3' photolabile group protected nucleotides can be recycled and directly used in the later coupling reactions. Unlike immobilized oligonucleotides having C-3' bound and C-5' at the terminal position which can only be used in hybridization for genetic anal., the immobilized oligonucleotides having C-5' bound and C-3' at the terminal position can be used as primers for polymerase mediated primer extension.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 45 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:565250 CAPLUS <<LOGINID::20090921>>
DN 135:148299
TI Human leucine-rich repeat protein 71 and its cDNA and use thereof
IN Mao, Yumin; Xie, Yi
PA Biodoor Gene Technology Ltd. Shanghai, Peop. Rep. China
SO PCT Int. Appl., 36 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001055374 A1 20010802 WO 2001-CN45 20010115 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,

SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1306975 A 20010808 CN 2000-111505 20000126 AU 2001029981 A 20010807 AU 2001-29981 20010115
PRAI CN 2000-111505 A 20000126 WO 2001-CN45 W 20010115
AB The invention provides cDNA sequences of a novel human leucine-rich repeat protein 71 cloned from human fetal brain. The invention also relates to constructing leucine-rich repeat protein 71 gene expression vectors to prep. recombinant leucine-rich repeat protein 71 protein using E.coli cells or eukaryotic cells. Methods of expressing and prepg. recombinant leucine-rich repeat protein 71 protein and its antibody are described. Methods of using leucine-rich repeat protein 71 gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 46 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:490370 CAPLUS <<LOGINID::20090921>>
DN 135:225720
TI Identification of novel cytokine-induced genes in pancreatic .beta.-cells by high-density oligonucleotide ***arrays***
AU Cardozo, Alessandra K.; Kruhoffer, Mogens; Leeman, Ruth; Orntoft, Torben; Eizirik, Decio L.
CS Gene Expression Unit, Diabetes Research Center, Vrije Universiteit Brussel, Brussels, B-1090, Belg.
SO Diabetes (2001), 50(5), 909-920 CODEN: DIAEAZ; ISSN: 0012-1797
PB American Diabetes Association
DT Journal
LA English
AB Type 1 diabetes is an autoimmune disease resulting from the selective destruction of insulin-producing .beta.-cells. Cytokines may contribute to pancreatic .beta.-cell death in type 1 diabetes. .beta.-Cell exposure to interleukin (IL)-1.beta. induces functional impairment, whereas .beta.-cell culture for 6-9 days in the presence of IL-1.beta. and interferon (IFN)-.gamma. leads to apoptosis. To clarify the mechanisms involved in these effects of cytokines, we studied the general pattern of cytokine-induced gene expression in .beta.-cells. Primary rat .beta.-cells were fluorescence-activated cell sorter-purified and exposed for 6 or 24 h to control condition, IL-1.beta. + IFN-.gamma., or IL-1.beta. alone (24 h only). Gene expression profile was analyzed in ***duplicate*** by ***oligonucleotide*** ***arrays*** . Nearly 3,000 transcripts were detected in controls and cytokine-treated .beta.-cells. Of these, 96 and 147 displayed changes in expression after 6 and 24 h, resp., of exposure to IL-1.beta. + IFN-.gamma., whereas 105 transcripts were modified after a 24-h exposure to IL-1.beta.. The cytokine-responsive genes were clustered according to their biol. functions. The major clusters obsd. were metab., signal transduction, transcription factors, protein synthesis/processing, hormones, and related receptors. These modifications in gene expression may explain some of the cytokine effects in .beta.-cells, such as decreased protein biosynthesis and insulin release. In addn., there was induction of diverse cytokines and chemokines; this suggests that .beta.-cells may contribute to mononuclear cell homing during insulitis. Several of the cytokine-induced genes are potentially regulated by the transcription factor NF-.kappa.B. Clarification of the function of the identified cytokine-induced gene patterns may unveil some of the mechanisms involved in .beta.-cell damage and repair in type 1 diabetes.
OSC.G 116 THERE ARE 116 CAPLUS RECORDS THAT CITE THIS RECORD (116 CITINGS)
RE.CNT 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 47 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:481370 CAPLUS <<LOGINID::20090921>>
DN 135:238727
TI Electronic transduction of polymerase or reverse transcriptase induced replication processes on surfaces: highly sensitive and specific detection of viral genomes
AU Patolsky, Fernando; Lichtenstein, Amir; Kotler, Moshe; Willner, Itamar
CS Inst. of Chem., The Hebrew Univ. of Jerusalem, Jerusalem, 91904, Israel
SO Angewandte Chemie, International Edition (2001), 40(12), 2261-2265 CODEN: ACIEF5; ISSN: 1433-7851
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
AB The authors address the development of ultrasensitive DNA-detection methods where in situ amplification proceeds on functionalized surfaces (electrodes or piezoelec. crystals) and the detection process is electronically transduced. The method enables the quant. anal. of viral DNA or RNA and may be adopted for parallel analyses on ***arrays*** . The surface polymerase-induced or reverse transcriptase stimulated formation of double-stranded DNA or RNA on the transducer, and the secondary amplification of the sensing process by the biocatalyzed pptn. of an insol. product are demonstrated. Electrochem. and microgravimetric QCM methods are used as electronic transduction means for the DNA detection. The process is exemplified by the anal. of the M13 mp8 (M13q) DNA (.apprx.300 copies per 10 .mu.L) and of the RNA of vesicular stomatitis virus (VSV; .apprx.60 copies per 10 .mu.L).
OSC.G 50 THERE ARE 50 CAPLUS RECORDS THAT CITE THIS RECORD (51 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 48 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:473245 CAPLUS <<LOGINID::20090921>>
DN 136:145693
TI Comparison of complex DNA mixtures with generic oligonucleotide microchips
AU Lebed, Julia B.; Chechetkin, Vladimir R.; Turygin, Alexander Y.; Shick, Valentin V.; Mirzabekov, Andrei D.
CS Joint Human Genome Program: Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, 117984, Russia
SO Journal of Biomolecular Structure & Dynamics (2001), 18(6), 813-823 CODEN: JBSDD6; ISSN: 0739-1102
PB Adenine Press
DT Journal
LA English
AB The reproducibility of melting curves for ***repeated*** hybridizations of target DNA with generic ***oligonucleotide*** microchips is shown exptl. to depend on the character of matching between fragments of target DNA and immobilized ***oligonucleotides*** . The reproducibility of melting curves is higher for the perfect match duplexes and decreases as the no. of mismatched pairs within duplexes increases. This effect was applied to the comparative anal. of complex DNA mixts. The authors developed a scheme in which the authors can identify

and discriminate between the probe oligonucleotides responsible for the distinctions between target DNA mixts. A scheme is illustrated by comparing DNA mixts. corresponding to V-D-J genes connected with populations of mRNAs CDR3 TCR Vb (T-cell receptor beta complementarity detg. region 3) from the thymus and pancreas of NOD mice. Our results demonstrate that generic microchips can be applied efficiently to the anal. of DNA mixts.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 49 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:391979 CAPLUS <<LOGINID::20090921>>
DN 135:1205
TI ***Arrays*** of double-stranded oligonucleotide VNTR probes for nucleic acid typing
IN Yeh, Homer R.; Wick, Charles H.
PA United States Dept. of the Army, USA
SO U.S., 24 pp., Cont. of U.S. Ser. No. 838,157, abandoned. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 6238866 B1 20010529 US 1999-246277 19990208
PRAI US 1996-15965 A1 19960416 US 1997-838157 B1 19970416
AB The present invention provides devices and methods for detecting or characterizing a nucleic acid analyte without requiring electrophoresis or the direct sequencing of analyte samples or analyte fragments. The device includes a panel or ***array*** of double stranded ***oligonucleotide*** probes immobilized on a solid support, each probe comprising a nucleotide sequence having a hypervariable no. of tandem ***repeat*** sequences. Desirably, the specificity of the probes is varied with the location on the panel or ***array*** . One strand of each probe is preferably anchored at one terminus to a solid support and the opposite terminus of a second strand is not so anchored. The probes and/or the analyte are labeled by one or more reporter moieties, designed, for example, to allow for visual or instrument based detection of hybridization events. The probes comprise a fragment of an Epstein-Barr virus genome spanning from about nucleotide 7421 to about nucleotide 8042.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 50 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:343652 CAPLUS <<LOGINID::20090921>>
DN 135:252463
TI Totally mutant telomeres: single-step mutagenesis of tandem repeat DNA sequences
AU Underwood, Dana Hager; McEachern, Michael J.
CS University of Georgia, Athens, GA, USA
SO BioTechniques (2001), 30(5), 934,936,938 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
AB A study was conducted to develop a method that can create a telomere composed solely of mutant repeats. Two sites were mutated simultaneously; one site is the desired mutation, and the second is a vector mutation that reduces the background of non-mutated plasmids. Results showed that ***oligonucleotide*** mutagenesis could be used to simultaneously alter every ***repeat*** in a tandem ***array*** of short ***repeats*** . The procedure allowed the generation of a totally mutant telomere in yeast. The technique could be used in systems such as Kluyveromyces lactis which contain long uniform telomeric repeats.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 51 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:320337 CAPLUS <<LOGINID::20090921>>
DN 134:363619
TI A factorial analysis of silanization conditions for the immobilization of oligonucleotides on glass surfaces
AU Halliwell, Catherine M.; Cass, Anthony E. G.
CS Department of Biochemistry Imperial College of Science Technology and Medicine, University of London, London, SW7 2AY, UK
SO Analytical Chemistry (2001), 73(11), 2476-2483 CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
AB The modification of glass surfaces with (3-mercaptopropyl)trimethoxysilane and the application of this to DNA chip technol. are described. A range of factors influencing the silanization method, and hence the no. of surface-bound, chem. active thiol groups, were investigated using a design of expt. approach based on anal. of variance. The no. of thiol groups introduced on glass substrates were measured directly using a specific radiolabel, [14C]cysteamine hydrochloride. For liq.-phase silanization, the no. of surface-bound thiol groups was found to be dependent on both postsilanization thermal curing and silanization time and relatively independent of silane concn., reaction temp., and sample pretreatment. Depending on the conditions used in liq.-phase silanization, (1.3-9.0) .times. 1012 thiol groups/cm2 on the glass samples were bound. The reliability and ***repeatability*** of liq.- and vacuum-phase silanization were also investigated. Eighteen-base ***oligonucleotide*** probes were covalently attached to the modified surfaces via a 3'-amino modification on the DNA and subsequent reaction with the crosslinking reagent N-(.gamma.-maleimidobutyryloxy) succinimide ester (GMBS). The resulting probe levels were detd. and found to be stoichiometric with that of the introduced thiol groups. These results demonstrate that silanization of glass surfaces under specific conditions, prior to probe attachment, is of great importance in the development of DNA chips that use the simple concept of the covalent attachment of presynthesized oligonucleotides to silicon oxide surfaces.
OSC.G 73 THERE ARE 73 CAPLUS RECORDS THAT CITE THIS RECORD (75 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 52 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:312014 CAPLUS <<LOGINID::20090921>>

DN 136:64938
TI Toward elucidating the global gene expression patterns of developing Arabidopsis: parallel analysis of 8 300 genes by a high-density oligonucleotide probe ***array***
AU Zhu, Tong; Budworth, Paul; Han, Bin; Brown, Devon; Chang, Hur-Song; Zou, Guangzhou; Wang, Xun
CS Torrey Mesa Research Institute, Inc., San Diego, CA, 92121, USA
SO Plant Physiology and Biochemistry (Paris, France) (2001), 39(3-4), 221-242 CODEN: PPBIEX; ISSN: 0981-9428
PB Editions Scientifiques et Medicales Elsevier
DT Journal
LA English
AB Arabidopsis thaliana has been widely used as a model system, in various aspects of biol. studies, such as genomics, genetics, cellular, developmental and mol. biol. In order to reveal the mol. events and regulatory networks controlling Arabidopsis development and responses to genetic and environmental changes, we designed and used a high-d. oligonucleotide probe ***array*** (GeneChip) to profile global gene expression patterns. The Arabidopsis oligonucleotide probe ***array*** consists of probes from 8 300 unique Arabidopsis genes, which covers approx. one-third of the genome. Global transcription profiles of A. thaliana in various developmental stages, and their responses to different environments were generated using this ***microarray*** , and archived. Here, we analyze data sets derived from nineteen independent expts. Constitutively and differentially expressed genes in seedlings, roots, leaves, inflorescences, flowers and siliques at different developmental stages were identified. Functions of these genes based on homologs were detd. and categorized. Our results provide insight into the coordinated transcriptional regulation of the genes during plant growth and development.
OSC.G 78 THERE ARE 78 CAPLUS RECORDS THAT CITE THIS RECORD (78 CITINGS)
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 53 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:300901 CAPLUS <<LOGINID::20090921>>
DN 134:321561
TI A method for the generation of repeat-depleted DNA
IN Speicher, Michael; Eils, Roland
PA Germany
SO PCT Int. Appl., 38 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001029252 A2 20010426 WO 2000-EP10268 20001018 WO 2001029252 A3 20020131 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI EP 1999-120618 A 19991018
AB The invention relates to a method for the generation of repeat-depleted DNA comprising amplifying repetitive template DNA by a first polymerase chain reaction (PCR), wherein the hybridization step is a low stringency hybridization step and a second PCR following the first PCR, wherein the hybridization step of said second PCR is a high stringency hybridization step. The repeat-depleted DNA obtained can be used as probe or cloned into vectors, plasmid, etc. Further, the invention relates to the application of the method in the generation of and hybridization with DNA libraries, DNA ***arrays*** or DNA blots.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 54 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:187083 CAPLUS <<LOGINID::20090921>>
DN 135:283870
TI E2Fs regulate the expression of genes involved in differentiation, development, proliferation, and apoptosis
AU Muller, Heiko; Bracken, Adrian P.; Vernell, Richard; Moroni, M. Cristina; Christians, Fred; Grassilli, Emanuela; Prosperini, Elena; Vigo, Elena; Oliner, Jonathan D.; Helin, Kristian
CS Department of Experimental Oncology, European Institute of Oncology, Milan, 20141, Italy
SO Genes & Development (2001), 15(3), 267-285 CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The retinoblastoma protein (pRB) and its two relatives, p107 and p130, regulate development and cell proliferation in part by inhibiting the activity of E2F-regulated promoters. High-d. oligonucleotide ***arrays*** were used to identify genes in which expression changed in response to activation of E2F1, E2F2, and E2F3. The E2Fs control the expression of several genes that are involved in cell proliferation. The E2Fs also regulate a no. of genes involved in apoptosis, differentiation, and development. These results provide possible genetic explanations to the variety of phenotypes obsd. as a consequence of a deregulated pRB/E2F pathway.
OSC.G 418 THERE ARE 418 CAPLUS RECORDS THAT CITE THIS RECORD (418 CITINGS)
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 55 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:72981 CAPLUS <<LOGINID::20090921>>
DN 135:176138
TI Chemical nanoprinting: a novel method for fabricating DNA microchips
AU Kumar, Anil; Liang, Zicai
CS Genomics Technology Unit, Center for Genomics Research, Karolinska Institutet, Stockholm, 17177, Swed.
SO Nucleic Acids Research (2001), 29(2), E2/1-E2/4 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB We have developed a novel cost-effective procedure, namely 'chem. nanoprinting', for oligonucleotide or cDNA chips manuf. In this thermo-controlled process, the oligonucleotides, covalently attached to a highly loaded 'master-chip' through disulfide bonds, are chem. transferred to the acrylamide layer mounted on a 'print-chip'. It is demonstrated here that multiple identical print-chips can be produced from a single master-chip. This duplication process is a few hundreds of times faster than any

existing methods and the speed of process and cost incurred are independent of the scale of the DNA chips.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 56 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:56246 CAPLUS <<LOGINID::20090921>>
DN 134:306943
TI Interaction of hnRNP A2/B1 Isoforms with Telomeric ssDNA and the in Vitro Function
AU Kamma, Hiroshi; Fujimoto, Mitsuo; Fujiwara, Masachika; Matsui, Miwa; Horiguchi, Hisashi; Hamasaki, Makoto; Satoh, Hiroaki
CS Institute of Basic Medical Sciences, University of Tsukuba, Ibaraki, 305-8575, Japan
SO Biochemical and Biophysical Research Communications (2001), 280(3), 625-630 CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal
LA English
AB Overexpression of heterogeneous nuclear ribonucleoprotein (hnRNP) A2/B1, esp. of B1 has been reported as a useful marker to detect cancers in early stage, although the biol. reason is not clear. A2/B1 proteins were previously reported to bind telomeric DNA repeats. Alternative splicing of A2/B1 gene produces abundant A2, less abundant B1, and testis-specific minor isoforms B0a and B0b. In this study, B1 and B0b that have the N-terminal 12 amino acid insertion were suggested to have higher affinities to telomeric single-stranded DNA (ssDNA) than A2 and B0a. Kinetic analyses using purified B1 and B0b indicated that they interact dynamically with a single ***array*** of telomeric repeats. Furthermore, functional assays demonstrated that B1 and B0b bind with telomeric repeats in a tandem fashion and protect them from a nuclease and promote telomerase activity. A2/B1 proteins, esp. B1 and B0b, may function as telomeric ssDNA-binding proteins in cancer and reproductive cells. (c) 2001 Academic Press.
OSC.G 34 THERE ARE 34 CAPLUS RECORDS THAT CITE THIS RECORD (34 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 57 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:909111 CAPLUS <<LOGINID::20090921>>
DN 134:52245
TI Detection of nucleic acids in samples using ordered ***arrays*** of probes by amplification of hybridization products
IN Lane, David J.; Farrell, Michael P.
PA Vysis, Inc., USA
SO U.S., 24 pp., Cont.-in-part of U.S. 5,837,466. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI US 6165714 A 20001226 US 1997-991675 19971216
US 5837466 A 19981117 US 1996-768177 19961216
JP 10293128 A 19981104 JP 1997-346496 19971216
PRAI US 1996-768177 A2 19961216
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The invention provides devices and methods for use in detecting nucleic acid analytes in samples. The devices each include a solid support to which is bound a two-dimensional distribution or field of nucleic acid probes that each bind to a nucleic acid analyte, which is detected by use of amplification methods. Ordered ***arrays*** of ***oligonucleotide*** probe/primers that include a sequence of an autocatalytic RNA such as a phage Q.beta. midivariant and that can be used in autocatalytic ***replication*** of hybridization products is described. The method uses a bound probe contg. part of the midivariant RNA of Q.beta. phage and a free probe contg. the remainder of the RNA. The bound and free probes hybridize adjacent to one another and can be joined together with an RNA ligase to form an intact Q.beta. midivariant analog that can then be amplified autocatalytically. Amplification can be detected by fluorescence of an intercalating dye.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 58 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:870504 CAPLUS <<LOGINID::20090921>>
DN 135:103182
TI Structural rearrangements and insertions of dispersed elements in pericentromeric alpha satellites occur preferably at kinkable DNA sites
AU Mashkova, Tamara D.; Oparina, Nina Yu.; Lacroix, Marie-Helene; Fedorova, Lyudmila I.; Tumeneva, Irina G.; Zinovieva, Olga L.; Kisselev, Lev L.
CS Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, 117984, Russia
SO Journal of Molecular Biology (2001), 305(1), 33-48 CODEN: JMOBAK; ISSN: 0022-2836
PB Academic Press
DT Journal
LA English
AB Centromeric region of human chromosome 21 comprises two long alphoid DNA ***arrays*** : the well homogenized and CENP-B box-rich .alpha.21-I and the .alpha.21-II, contg. a set of less homogenized and CENP-B box-poor subfamilies located closer to the short arm of the chromosome. Continuous alphoid fragment of 100 monomers bordering the non-satellite sequences in human chromosome 21 was mapped to the pericentromeric short arm region by fluorescence in situ hybridization (.alpha.21-II locus). The alphoid sequence contained several rearrangements including five large deletions within monomers and insertions of three truncated L1 elements. No binding sites for centromeric protein CENP-B were found. We analyzed sequences with alphoid/non-alphoid junctions selectively screened from current databases and revealed various rearrangements disrupting the regular tandem alphoid structure, namely, deletions, ***duplications*** , inversions, expansions of short ***oligonucleotide*** motifs and insertions of different dispersed elements. The detailed anal. of more than 1100 alphoid monomers from junction regions showed that the vast majority of structural alterations and joinings with non-alphoid DNAs occur in alpha satellite families lacking CENP-B boxes. Most analyzed events were found in sequences located toward the edges of the centromeric alphoid ***arrays*** . Different dispersed elements were inserted into alphoid DNA at kinkable dinucleotides (TG, CA or TA) situated between pyrimidine/purine tracks. DNA rearrangements resulting from

different processes such as recombination and replication occur at kinkable DNA sites alike insertions but irresp. of the occurrence of pyrimidine/purine tracks. It seems that kinkable dinucleotides TG, CA and TA are part of recognition signals for many proteins involved in recombination, replication, and insertional events. Alphoid DNA is a good model for studying these processes. (c) 2001 Academic Press.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 59 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:774172 CAPLUS <<LOGINID::20090921>>
DN 135:103027
TI Oligonucleotide ***microarray*** based detection of repetitive sequence changes
AU Hacia, Joseph G.; Edgemon, Keith; Fang, Nicole; Mayer, R. Aeryn; Sudano, Dominick; Hunt, Nathaniel; Collins, Francis S.
CS National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, 20892, USA
SO Human Mutation (2000), 16(4), 354-363 CODEN: HUMUE3; ISSN: 1059-7794
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Prior studies of ***oligonucleotide*** ***microarray*** -based mutational anal. have demonstrated excellent sensitivity and specificity except in circumstances where a frameshift mutation occurs in the context of a short ***repeated*** sequence. To further evaluate this circumstance, a series of nucleic acid samples having heterozygous mutations within repetitive BRCA1 sequence tracts was prepd. and evaluated. These mutations included single nucleotide insertions and deletions in homopolymer runs, insertions and deletions of trinucleotide repeats, and duplications. Two-color comparative hybridization expts. were used wherein wild type ref. and test targets are co-hybridized to ***microarrays*** designed to screen the entire BRCA1 coding sequence for all possible sequence changes. Mutations in simulated heterozygote samples were detected by observing relative losses of test target hybridization signal to select perfect match oligonucleotide probes. While heterozygous mutations could be readily distinguished above background noise in 9/19 cases, it was not possible to detect alterations in a poly dA/dT tract, small triplet repeat expansions, and a 10 bp direct repeat. Unexpectedly, samples contg. (GAT)3 triplet repeat expansions showed significantly higher affinity toward specific perfect match probes relative to their wild type counterparts. Therefore, markedly increased as well as decreased test sample hybridization to perfect match probes should be used to raise a suspicion of repetitive sequence changes.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 60 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:601969 CAPLUS <<LOGINID::20090921>>
DN 134:323965
TI Analysis of telomere length in Dolly, a sheep derived by nuclear transfer
AU Shiels, Paul G.; Kind, Alexander J.; Campbell, Keith H. S.; Wilmut, Ian; Waddington, David; Colman, Alan; Schnieke, Angelika E.
CS PPL Therapeutics, Roslin, UK
SO Cloning (1999), 1(2), 119-125 CODEN: CLONFB; ISSN: 1520-4553
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB We have used a (TTAGGG) ***oligonucleotide*** probe to demonstrate that ovine telomeres are composed of (TTAGGG) ***repeat*** ***arrays*** and to compare the terminal restriction fragment lengths of sheep derived by natural mating and nuclear transfer. Here we show that ovine somatic telomeres decrease in length with age, and that Dolly, derived by the transfer of 6-yr-old adult somatic nucleus, exhibits diminished terminal restriction fragment lengths. The decrease is consistent with the age of the donor tissue and telomere erosion during in vitro culture. Nuclear transfer does not restore telomere lengths. Dolly otherwise appears physiol. and phenotypically normal for her breed and age. We further report on apparent telomere lengthening in sheep, occurring during the first year in naturally derived lambs.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 61 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:398494 CAPLUS <<LOGINID::20090921>>
DN 133:291882
TI Decreased expression of striatal signaling genes in a mouse model of Huntington's disease
AU Luthi-Carter, Ruth; Strand, Andrew; Peters, Nikki L.; Solano, Steven M.; Hollingsworth, Zane R.; Menon, Anil S.; Frey, Ariel S.; Spektor, Boris S.; Penney, Ellen B.; Schilling, Gabriele; Ross, Christopher A.; Borchelt, David R.; Tapscott, Stephen J.; Young, Anne B.; Cha, Jang-Ho J.; Olson, James M.
CS Department of Neurology, Massachusetts General Hospital, Boston, MA, 02114, USA
SO Human Molecular Genetics (2000), 9(9), 1259-1271 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB To understand gene expression changes mediated by a polyglutamine ***repeat*** expansion in the human huntingtin protein, the authors used ***oligonucleotide*** DNA ***arrays*** to profile .apprx.6000 striatal mRNAs in the R6/2 mouse, a transgenic Huntington's disease (HD) model. The authors found diminished levels of mRNAs encoding components of the neurotransmitter, calcium and retinoid signaling pathways at both early and late symptomatic time points (6 and 12 wk of age). The authors obsd. similar changes in gene expression in another HD mouse model (N171-82Q). These results demonstrate that mutant huntingtin directly or indirectly reduces the expression of a distinct set of genes involved in signaling pathways known to be crit. to striatal neuron function.
OSC.G 339 THERE ARE 339 CAPLUS RECORDS THAT CITE THIS RECORD (340 CITINGS)
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 62 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2000:384469 CAPLUS <<LOGINID::20090921>>
DN 133:13387
TI Using the specific interactions between nucleic acids to create complementary copies of ***arrays*** of oligonucleotides
IN Von Kiedrowski, Gunter; Furste, Jens Peter; Klussmann, Sven; Klein, Thomas
PA Noxxon Pharma A.-G., Germany
SO PCT Int. Appl., 46 pp. CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2000032809 A2 20000608 WO 1999-DE3856 19991126 WO 2000032809 A3 20001019 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG DE 19854946 A1 20000608 DE 1998-19854946 19981127 DE 19854946 C2 20020103 EP 1135527 A2 20010926 EP 1999-962118 19991126 EP 1135527 B1 20021016 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO JP 2002531098 T 20020924 JP 2000-585440 19991126 AT 226258 T 20021115 AT 1999-962118 19991126 ES 2186427 T3 20030501 ES 1999-962118 19991126 US 20020022275 A1 20020221 US 2001-866513 20010525 US 6534271 B2 20030318
PRAI DE 1998-19854946 A 19981127 WO 1999-DE3856 W 19991126
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The invention relates to a method for cloning and copying genetic material on surfaces as well as copying biol. material insofar as it, in a broader sense, can be classified in a ligand receptor system. The invention thus relates, in particular, to a method for propagating ligands and receptors on at least two surfaces which comprises one or several of the following cycles: immobilizing a ligand on a first surface of a solid phase; adding a soln. of receptors and binding complementary receptors to the ligands; transferring the receptor to an addnl. surface and immobilizing the receptor at that location; attaching an addnl. ligand to the immobilized receptor; transferring the ligand to a surface and immobilizing the same at that location. Nucleic acids are also understood as a ligand/receptor system.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 63 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:795999 CAPLUS <<LOGINID::20090921>>
DN 132:45816
TI Restriction enzyme gene discovery method using cassette ***arrays*** containing repeat sequences flanking variable open reading frames
IN Raleigh, Elisabeth A.; Vaisvila, Romualdas; Morgan, Richard D.
PA New England Biolabs, Inc., USA
SO PCT Int. Appl., 97 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 9964632 A1 19991216 WO 1999-US13295 19990611 W: JP, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE EP 1086244 A1 20010328 EP 1999-927501 19990611 R: DE, FR, GB JP 2002517260 T 20020618 JP 2000-553622 19990611
PRAI US 1998-89086P P 19980612 US 1998-89101P P 19980612 WO 1999-US13295 W 19990611
AB The invention enables direct cloning of intact genes, with a high probability that the orientation of expression is known in advance, and with a low probability of being assocd. with extraneous possibly toxic genes. The invention is particularly directed to obtaining genes encoded in DNA cassettes comprised of repeat sequences flanking variable open reading frames. The invention encompasses obtaining such cassette-encoded genes using ***oligonucleotides*** hybridizing to the ***repeated*** elements, cloning them and expressing them. Expression may employ tightly regulated vectors and useful strains disclosed. Methods for identifying restriction endonuclease and DNA methyltransferase genes in the absence of prior information about the sequences or biochem. specificities of these are also disclosed. Besides of restriction enzymes genes among the genes to be found in cassette ***arrays*** of invention are genes for adhesins, small-mol. modifying enzymes, and specific toxins.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 64 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:683615 CAPLUS <<LOGINID::20090921>>
DN 132:45502
TI Maskless fabrication of light-directed oligonucleotide ***microarrays*** using a digital micromirror ***array***
AU Singh-Gasson, Sangeet; Green, Roland D.; Yue, Yongjian; Nelson, Clark; Blattner, Fred; Sussman, Michael R.; Cerrina, Franco
CS Cent. NanoTechnol., Dep. Electrical and Computer Eng., Univ. Wisconsin, Madison, WI, 53706, USA
SO Nature Biotechnology (1999), 17(10), 974-978 CODEN: NABIF9; ISSN: 1087-0156
PB Nature America
DT Journal
LA English
AB Oligonucleotide ***microarrays*** , also called "DNA chips," are currently made by a light-directed chem. that requires a large no. of photolithog. masks for each chip. Here we describe a maskless ***array*** synthesizer (MAS) that replaces the chrome masks with virtual masks generated on a computer, which are relayed to a digital micromirror ***array*** . A 1:1 reflective imaging system forms an UV image of the virtual mask on the active surface of the glass substrate, which is mounted in a flow cell reaction chamber connected to a DNA synthesizer. Programmed chem. coupling cycles follow light exposure, and these steps are ***repeated*** with different virtual masks to grow desired ***oligonucleotides*** in a selected pattern. This instrument has been used to synthesize oligonucleotide ***microarrays*** contg. more than 76,000 features measuring 16 .mu.m2. The

oligonucleotides were synthesized at high repetitive yield and, after hybridization, could readily discriminate single-base pair mismatches. The MAS is adaptable to the fabrication of DNA chips contg. probes for thousands of genes, as well as any other solid-phase combinatorial chem. to be performed in high-d. ***microarrays*** .
OSC.G 370 THERE ARE 370 CAPLUS RECORDS THAT CITE THIS RECORD (372 CITINGS)
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 65 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:673414 CAPLUS <<LOGINID::20090921>>
DN 132:10635
TI Instability characteristics of trinucleotide (CAG) repeat tracts in Escherichia coli
AU Hanrahan, Vickie; George, Peter M.; Kennedy, Martin A.
CS Department of Pathology, Christchurch School of Medicine, Christchurch, N. Z.
SO Journal of Biochemistry, Molecular Biology and Biophysics (1999), 3(2), 117-125 CODEN: JBMBF6; ISSN: 1025-8140
PB Harwood Academic Publishers
DT Journal
LA English
AB The instability of trinucleotide CAG repeat tracts propagated in bacterial plasmids is thought to be mechanistically related to the process of trinucleotide repeat expansion obsd. in several inherited human diseases. We systematically explored the instability of CAG(n) tracts of different length in E. coli, and obsd. that changes in repeat length almost never occurred when the ***array*** was less than 32 trinucleotides long. This length is close to the upper size limit obsd. for stability of the CAG repeat implicated in Huntington's disease. As the repeat ***arrays*** increased beyond this length, the frequency and size of expansions and deletions increased, resembling changes seen at the Huntington's disease locus in humans. This supports the notion that instability of large CAG(n) repeats is due to an intrinsic property of such DNA sequences and confirms that E. coli is a relevant model in which to explore the genomic instability underlying inherited trinucleotide repeat disease in humans.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 66 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:635420 CAPLUS <<LOGINID::20090921>>
DN 131:253328
TI Methods for the generation of sequence signatures from nucleic acids and DNA fingerprinting enhancement using mini-hairpin primers and electrophoresis
IN Caetano-Anolles, Gustavo
PA USA
SO U.S., 24 pp., Cont. of U.S. Ser. No. 139,459. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 7 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 5962221 A 19991005 US 1995-489269 19950609 US 5413909 A 19950509 US 1993-6380 19930119 US 6074818 A 20000613 US 1993-139459 19931020 WO 9641893 A1 19961227 WO 1996-US10042 19960607 W: AU, CA, DE, JP, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM AU 9662728 A 19970109 AU 1996-62728 19960607
PRAI US 1993-6380 A2 19930119 US 1993-139459 A2 19931020 US 1990-573627 B1 19900824 US 1991-676869 B2 19910328 US 1995-489269 A 19950609 WO 1996-US10042 W 19960607
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB Novel oligonucleotides for amplification and profiling of nucleic acid templates are disclosed. Enhancements of nucleic acid fingerprinting methods are disclosed. Mini-hairpin primers, single sequence ***repeat*** (SSR) primers, extension strands, ***oligonucleotide*** ***arrays*** , and capillary electrophoresis methods are described. Primers with short (3-4 base) single-stranded regions and a hairpin loop domain were found to improve accuracy of the amplification. The modification of the DAF (DNA amplification fingerprinting) technol. to increase the detection and/or visualization of polymorphisms, primarily by modifications of the sepn. step is included.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 67 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:537406 CAPLUS <<LOGINID::20090921>>
DN 132:33727
TI Patterns of instability of expanded CAG repeats at the ERDA1 locus in general populations
AU Deka, Ranjan; Sun, Guangyun; Wiest, Jonathan; Smelser, Diane; Chunhua, Su; Zhong, Yixi; Chakraborty, Ranajit
CS Department of Environmental Health, University of Cincinnati, Cincinnati, OH, 45267-0056, USA
SO American Journal of Human Genetics (1999), 65(1), 192-198 CODEN: AJHGAG; ISSN: 0002-9297
PB University of Chicago Press
DT Journal
LA English
AB A highly polymorphic CAG repeat locus, ERDA1, was recently described on human chromosome 17q21.3, with alleles as large as 50-90 repeats and without any disease assocn. in the general population. The authors have studied allelic distribution at this locus in five human populations and have characterized the mutational patterns by direct observation of 731 meioses. The data show that large alleles (.gtoreq.40 CAG repeats) are generally most common in Asian populations, less common in populations of European ancestry, and least common among Africans. The authors have obsd. a high intergenerational instability (46.3%) of the large alleles. Although the mutation rate is not dependent on parental sex, paternal transmissions have predominantly resulted in contractions, whereas maternal transmissions have yielded expansions. Within this class of large alleles, the mutation rate increases concomitantly with increasing allele size, but the magnitude of repeat size change does not depend on the size of the progenitor allele. Sequencing of specific alleles reveals that the intermediate-sized alleles (30-40 repeats) have CAT/CAC interruptions within the CAG-repeat ***array*** . These results indicate that expansion and instability of trinucleotide repeats are not exclusively disease-assocd. phenomena. The implications of the existence of massively expanded alleles in the general populations are not yet understood.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 68 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:458573 CAPLUS <<LOGINID::20090921>>
DN 131:317137
TI Oligonucleotides as inhibitors of human immunodeficiency virus
AU Field, A. Kirk
CS Department of Pharmacology and Toxicology, University of Massachusetts Medical Center, Worcester, MA, 01655, USA
SO Current Opinion in Molecular Therapeutics (1999), 1(3), 323-331 CODEN: CUOTFO; ISSN: 1464-8431
PB Current Drugs Ltd.
DT Journal; General Review
LA English
AB A review with 93 refs. Inhibition of human immunodeficiency virus (HIV) ***replication*** by ***oligonucleotides*** is a complex process and may be implemented by an ***array*** of antiviral mechanisms. These include inhibition of virus adsorption to the host cell, inhibition of transcription via antisense or as the result of triple helix formation, and inhibition of viral encoded enzymes such as reverse transcriptase and integrase. Since the particular mechanism of HIV inhibition depends on the oligonucleotide (ON) sequence and the ON chem. modifications, the design and synthesis of potent HIV inhibitors has been an important and rewarding focus of ON research. In this era of great concern that HIV may rapidly display resistance to any antiviral compd. with one mechanism of viral inhibition, oligonucleotides are potentially attractive alternatives for therapy. Several ONs have entered clin. evaluation in AIDS patients. At present Zintevir, which inhibits both HIV adsorption and HIV integrase, is in phase I/II clin. trials.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 93 THERE ARE 93 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 69 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1998:724671 CAPLUS <<LOGINID::20090921>>
DN 130:110544
TI Antiviral Oligo- and Polyribonucleotides Containing Selected Triazolo[2,3-a]purines
AU Tutonda, Mayoka G.; Buckheit, Robert W. ,Jr.; Agrawal, Vijai K.; Broom, Arthur D.
CS Department of Medicinal Chemistry, University of Utah, Salt Lake City, UT, 84112-9453, USA
SO Journal of Medicinal Chemistry (1998), 41(25), 4958-4964 CODEN: JMCMAR; ISSN: 0022-2623
PB American Chemical Society
DT Journal
LA English
AB Several amphipathic (hydrophobic base, hydrophilic backbone) polyribonucleotides have recently been shown to have potent antiviral activity against HIV and human cytomegalovirus (HCMV). The working hypothesis developed during these studies was that the ability to form an ordered, non-hydrogen-bonded ***array*** in soln. was an important criterion for activity. To explore further the role of structure and mol. size on the inhibition of virus ***replication*** , one new polynucleotide and two 32-mer ***oligonucleotides*** based on the triazolo[2,3-a]purine ring system have now been prepd. High-mol.-wt. polynucleotide (PTPR) and sulfur-contg. 32-mer (TTPR) were moderately active against HIV but showed greater potency against HDMV than ganciclovir.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 70 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1998:571896 CAPLUS <<LOGINID::20090921>>
DN 129:311343
OREF 129:63421a,63424a
TI Repeat expansion-detection analysis of telomeric uninterrupted (TTAGGG)n ***arrays***
AU Sirugo, Giorgio; Kidd, Kenneth K.
CS Department of Genetics, Yale University School of Medicine, New Haven, CT, 06520-8005, USA
SO American Journal of Human Genetics (1998), 63(2), 648-651 CODEN: AJHGAG; ISSN: 0002-9297
PB University of Chicago Press
DT Journal
LA English
AB The authors describe a method for repeat expansion detection, which gives a direct measure of the actual size of the longest uninterrupted TTAGGG repeat in the genome. The assay uses genomic DNA as a template for annealing and ligation of ***repeat*** -specific ***oligonucleotides*** , and does not require flanking sequence detn. or single-copy probes.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 71 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1998:474002 CAPLUS <<LOGINID::20090921>>
DN 129:105212
OREF 129:21521a,21524a
TI Detection of nucleic acids in samples using ordered ***arrays*** of probes by amplification of hybridization products
IN Lane, David J.; Farrell, Michael P.
PA Vysis, Inc., USA
SO Eur. Pat. Appl., 25 pp. CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI EP 853129 A2 19980715 EP 1997-310133 19971216 EP 853129 A3 19990707 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO US 5837466 A 19981117 US 1996-768177 19961216 JP 10293128 A 19981104 JP 1997-346496 19971216
PRAI US 1996-768177 A 19961216
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB Ordered ***arrays*** of ***oligonucleotide*** probe/primers that include a sequence of an autocatalytic RNA such as a phage Q.beta. midivariant and that can be used in autocatalytic ***replication*** of hybridization products is described. The method uses a bound probe contg. part of the midivariant RNA of Q.beta. phage and a free probe contg. the remainder of the RNA. The bound and free probes hybridize adjacent to one another and can be joined together with an RNA

ligase to form an intact Q.beta. midivariant analog that can then be amplified autocatalytically. Amplification can be detected by fluorescence of an intercalating dye.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L9 ANSWER 72 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1998:239312 CAPLUS <<LOGINID::20090921>>
DN 128:279546
OREF 128:55245a,55248a
TI Nucleic acid sequencing by adaptor ligation
IN Schmidt, Gunter; Thompson, Andrew Hugin
PA Brax Genomics Limited, UK; Schmidt, Gunter; Thompson, Andrew Hugin
SO PCT Int. Appl., 94 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 9815652 A1 19980416 WO 1997-GB2734 19971006 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG AU 9745663 A 19980505 AU 1997-45663 19971006
PRAI GB 1996-20769 A 19961004 WO 1997-GB2734 W 19971006
AB A method for sequencing nucleic acid is provided. A target nucleic acid population is obtained comprising nucleic acid fragments in which each fragment is present in a unique amt. and bears at one end a sticky end sequence of predetd. length and unknown sequence. The other end of each fragment is protected. Each of the fragments is sequenced by (i) contacting the fragments with an ***array*** of adaptor oligonucleotides under hybridization conditions, each adaptor oligonucleotide bearing a label, a sequencing enzyme recognition site, and a known unique base sequence of same predetd. length as the sticky end sequence, the ***array*** contg. all possible base sequences of that predetd. length; removing any unhybridized adaptor ***oligonucleotide*** and recording the quantity of any hybridized adaptor ***oligonucleotide*** by detection of the label, then ***repeating*** the cycle, until all of the adaptors in the ***array*** have been tested; (ii) contacting the hybridized adaptor ***oligonucleotides*** with a sequencing enzyme which binds to the recognition site and cuts the fragment to expose a new sticky end sequence which is contiguous with or overlaps the previous sticky end sequence. Steps (i) and (ii) are repeated for a sufficient no. of times and the sequence of the fragment detd. by comparing the quantities recorded for each sticky end sequence. The process does not require traditional gel methods to acquire sequence information. Since the entire process takes place in soln. and is an iterative process, the steps involved could be performed by a liq.-handling robot or a microfluidics system.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 73 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:412453 CAPLUS <<LOGINID::20090921>>
DN 127:61340
OREF 127:11625a,11628a
TI Spatially addressable ligation assays: application of oligonucleotide ***arrays*** to DNA fingerprinting
AU Pritchard, Clare E.; Southern, Edwin M.
CS Department of Biochemistry, University of Oxford, Oxford, OX1 3QU, UK
SO Innovation and Perspectives in Solid Phase Synthesis & Combinatorial Libraries: Peptides, Proteins and Nucleic Acids--Small Molecule Organic Chemical Diversity, Collected Papers, International Symposium, 4th, Edinburgh, Sept. 12-16, 1995 (1996), Meeting Date 1995, 499-502. Editor(s): Epton, Roger. Publisher: Mayflower Scientific, Birmingham, UK. CODEN: 64ONA9
DT Conference
LA English
AB Oligonucleotide ***arrays*** can be synthesized by solid phase methods. These ***arrays*** can be used in ligation assays to detect base substitutions in DNA. Also, a novel ***array*** can be synthesized and used, with a DNA ligation assay, to measure the length of short tandem repeats (STR) in DNA.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L9 ANSWER 74 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:132843 CAPLUS <<LOGINID::20090921>>
DN 126:140567
OREF 126:27051a,27054a
TI Methods for the generation of sequence signatures from nucleic acids and DNA fingerprinting enhancement using mini-hairpin primers and electrophoresis
IN Caetano-Anolles, Gustavo
PA University of Tennessee Research Corporation, USA
SO PCT Int. Appl., 67 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 7 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 9641893 A1 19961227 WO 1996-US10042 19960607 W: AU, CA, DE, JP, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM US 5962221 A 19991005 US 1995-489269 19950609 AU 9662728 A 19970109 AU 1996-62728 19960607
PRAI US 1995-489269 A 19950609 US 1993-6380 A2 19930119 US 1993-139459 A2 19931020 WO 1996-US10042 W 19960607
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB Novel oligonucleotides for amplification and profiling of nucleic acid templates are disclosed. Enhancements of nucleic acid fingerprinting methods are disclosed. Mini-hairpin primers, single sequence ***repeat*** (SSR) primers, extension strands, ***oligonucleotide*** ***arrays*** , and electrophoresis methods are described. Arbitrary Signature for Amplification profiles (ASAPs) are included.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 75 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:103677 CAPLUS <<LOGINID::20090921>>

DN 126:153621
OREF 126:29599a,29602a
TI The iteron bases and spacers of the P1 replication origin contain information that specifies the formation of a complex structure involved in initiation
AU Brendler, Therese G.; Abeles, Ann L.; Reaves, Lucretia D.; Austin, Stuart J.
CS Gene Regulation and Chromosome Biology Laboratory, ABL-Basic Research Program, NCI-Frederick Cancer Research and Development Center, Frederick, MD, 21702-1201, USA
SO Molecular Microbiology (1997), 23(3), 559-567 CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell
DT Journal
LA English
AB The origin of replication of the P1 plasmid contains five direct, imperfect repeats (iterons) of a 19bp sequence that binds the P1-encoded RepA initiator protein. RepA binding to these iterons triggers origin initiation and represses transcription from the repA promoter that is nested within the iterons. The origin iterons were replaced with ligated ***oligonucleotides*** that insert five perfect 19bp ***repeats*** with identical spacer sequences. This eliminates the natural variation in the iteron and spacer sequences and removes the repA promoter. The reconstructed origin is functional, showing that the repA promoter is not essential for origin function. The method used to make the reconstructed origin allows substitution of identical iterons with altered sequence or spacer length. Single changes of conserved iteron bases gave reduced or non-existent origin activity, as did an increase in spacer length. Like the wild type, most of these mutant ***arrays*** retain avid primary binding activity for the RepA protein. However, although the wild-type ***arrays*** readily form a mature complex in which all iterons are satd., the most replication-defective mutants were completely unable to do this, even at very high RepA concns. It appears that iteron spacing and contacts involving at least three of the conserved iteron bases play an important role in the assembly of the mature structure in which all sites are occupied. A model is presented in which an allosteric interaction between the DNA site and protein is needed for the satd., mature complex required for initiation.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L9 ANSWER 76 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:48892 CAPLUS <<LOGINID::20090921>>
DN 126:55937
OREF 126:10927a,10930a
TI Repeat nucleic acid detection by hybridization with an ***array*** of probes, heteroduplex cleavage with single-strand-specific nuclease, and 3'-hydroxyl extension with a polymerase
IN Smith, Cassandra L.; Yaar, Ron; Szafranski, Przemyslaw; Cantor, Charles R.
PA Trustees of Boston University, USA
SO PCT Int. Appl., 38 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 9636731 A2 19961121 WO 1996-US6527 19960520 WO 9636731 A3 19970206 W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML US 5753439 A 19980519 US 1995-446102 19950519 CA 2221467 A1 19961121 CA 1996-2221467 19960520 AU 9662486 A 19961129 AU 1996-62486 19960520 EP 827551 A2 19980311 EP 1996-921212 19960520 EP 827551 B1 19990811 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI AT 183244 T 19990815 AT 1996-921212 19960520
PRAI US 1995-446102 A 19950519 WO 1996-US6527 W 19960520
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The invention relates to methods for rapidly detg. the sequence and/or length of a target sequence. The target sequence may be a series of known or unknown repeat sequences which are hybridized to an ***array*** of probes. The hybridized ***array*** is digested with a single-strand nuclease and free 3'-hydroxyl groups extended with a nucleic acid polymerase. Nuclease cleaved heteroduplexes can be easily distinguished from nuclease uncleaved heteroduplexes by differential labeling. Probes and target can be differentially labeled with detectable labels. Matched target can be detected by cleaving resulting loops from the hybridized target and creating free 3-hydroxyl groups. These groups are recognized and extended by polymerases added into the reaction system which also adds or releases one label into soln. These methods can be used to detect characteristic nucleic acid sequences, to det. target sequence and to screen for genetic defects and disorders. Assays can be conducted on solid surfaces allowing for multiple reactions to be conducted in parallel and, if desired, automated. The method and the specificity and efficiency of S1 nuclease was demonstrated with ***oligonucleotides*** contg. eight GAC ***repeats*** , eight CTG ***repeats*** , and six CTG ***repeats*** , resp. To det. the extent of expansion of trinucleotide ***repeats*** in myotonic dystrophy, the DNA region contg. the ***repeats*** was amplified and isolated by PCR, and then analyzed using a set of ***oligonucleotide*** probes contg. the 20-bp 5' and 3' sequences complementary to the sequence flanking the trinucleotide ***repeat*** region as well as an internal trinucleotide ***repeat*** between the 5' and 3' sequences.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 77 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1996:381436 CAPLUS <<LOGINID::20090921>>
DN 125:77973
OREF 125:14655a,14658a
TI Terminal long tandem repeats in chromosomes from Chironomus pallidivittatus
AU Lopez, Casimiro C.; Nielsen, Lena; Edstroem, Jan-Erik
CS Department Genetics, Lund University, Lund, S-22362, Swed.
SO Molecular and Cellular Biology (1996), 16(7), 3285-3290 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB We provide evidence that a chromosome end in the dipteran Chironomus pallidivittatus contains 340-bp tandem repeats reaching the extreme terminus of the chromosome. After adding

synthetic ***oligonucleotide*** tails to DNA extd. from the microdissected right end of the 4th chromosome, we could demonstrate that the blocks of ***repeats*** were tailed at only one end, the chromosome terminus, the interior of the ***arrays*** being unavailable for tailing. Using PCR, we furthermore showed that the added tails were connected to 340-bp repeat DNA directly, i.e., without intervening DNA of any other kind. Using plasmid controls, we could also make certain that we did not amplify rare or nonrepresentative DNA termini.
OSC.G 52 THERE ARE 52 CAPLUS RECORDS THAT CITE THIS RECORD (52 CITINGS)

L9 ANSWER 78 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1996:95092 CAPLUS <<LOGINID::20090921>>
DN 124:137780
OREF 124:25427a,25430a
TI ***Oligonucleotide*** ***repeat*** ***arrays*** for hybridization assay of short tandem ***repeat*** sequences
IN Caskey, Charles Thomas; Matson, Robert S.; Coassin, Peter J.; Rampal, Jang B.
PA Beckman Instruments, Inc., USA
SO PCT Int. Appl., 60 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 9530774 A1 19951116 WO 1995-US4899 19950424 W: AU, JP RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE AU 9523601 A 19951129 AU 1995-23601 19950424 EP 758403 A1 19970219 EP 1995-917612 19950424 EP 758403 B1 19980624 R: DE, FR, GB US 5981185 A 19991109 US 1997-863639 19970528
PRAI US 1994-239475 A 19940505 WO 1995-US4899 W 19950424
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB A solid support-based hybridization assay is provided which allows for the systematic and reproducible anal. of ***repeat*** and tandem ***repeat*** ***oligonucleotide*** sequences of DNA and RNA by hybridization to a reverse dot blot ***array*** comprising strings of such ***repeats*** complementary to those found in particular nucleic acid targets (e.g. analyte PCR product). An addressable library (i.e., an indexed set) of complementary repeats is synthesized on a suitable support. Preferably, the support comprises a low fluorescent background support, thereby facilitating the use of non-radioisotopic modes of detection (such as fluorescence of chemiluminescence); particularly suitable in this regard is an aminated polypropylene support or similar material. Preferred ***arrays*** permit screening of DNA and RNA samples for complete sets of particular types of nucleotide repeat sequences (e.g., all nucleotide doublet or triplet repeats). Thus, a vertical ***array*** of 64 ***oligonucleotides*** was constructed, consisting of 60 triplet tandem ***repeat*** sequences (21mers) and 4 dinucleotide tandem ***repeat*** sequences (20mers) on a polypropylene substrate. This ***array*** was designed to represent trinucleotide repeats by all 3 possible frames in 3'.fwdarw.5' direction as well as in the reverse direction. The obtained band pattern in this reverse blotting system provided qual. precise identification of previously known STRs in DNA samples of various complexities between 21-34,977 bp. Moreover, there was no random or cross hybridization to unspecific sequences obsd.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 79 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1995:201825 CAPLUS <<LOGINID::20090921>>
DN 123:2451
OREF 123:543a,546a
TI Molecular cloning and analysis of one member of a polymorphic family of GACA-hybridizing DNA repeats in tomato
AU Phillips, W. J.; Chapman, C. G. D.; Jack, P. L.
CS Plant Breeding International Cambridge Limited, Cambridge, CB2 2LQ, UK
SO Theoretical and Applied Genetics (1994), 88(6-7), 845-51 CODEN: THAGA6; ISSN: 0040-5752
DT Journal
LA English
AB Simple sequence ***repeat*** ***oligonucleotides*** were used to probe the tomato genome for elements displaying variability amongst com. cultivars. The oligonucleotide (GACA)4 was found to be particularly informative on genotype screening blots, hybridizing to a highly polymorphic family of elements, and was used to clone one such member from a lambda library. The GACA-hybridization was localised to a 1.3-kb HinfI fragment within the original 15-kb lambda insert. This 1,349-bp subclone (pT-GACA-2:1.3) was found to probe 27 Californian processing varieties and found to be capable of distinguishing all from each other, thus demonstrating its utility as a genetic fingerprinting probe for cultivar identification. Hybridization occurred to approx. 10 major high mol. wt. (>4-kb) bands, most of which segregated independently in F2 populations, as well as a large no. of less clearly resolvable smaller fragments. Sequence anal. of the cloned element reveals that it is almost entirely composed of GACA or GATA repeats. These tetranucleotides are organized into distinct repetitive domains, consisting either of tandem ***arrays*** of each tetranucleotide or interspersions of GACA and GATA to form dodecanucleotides that are then further repeated. The boundaries between domains contain sufficient departures from the consensus repeat to allow construction of unique polymerase chain reaction (PCR) primers. Amplification from two such contiguous regions identifies length variation in both, thus yielding a genotype screen appropriate for high-throughput applications, such as assessment of purity in F1 hybrid seed lots.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L9 ANSWER 80 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1994:552587 CAPLUS <<LOGINID::20090921>>
DN 121:152587
OREF 121:27493a,27496a
TI Quantitative Analysis of Macromolecular Conformational Changes Using Agarose Gel Electrophoresis: Application to Chromatin Folding
AU Fletcher, Terace M.; Serwer, Philip; Hansen, Jeffrey C.
CS Health Science Center, University of Texas, San Antonio, TX, 78284-7760, USA
SO Biochemistry (1994), 33(36), 10859-63 CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English

AB Quant. anal. of chromatin electrophoretic mobility (.mu.) in agarose gels provides a measure of three structural parameters: av. surface elec. charge d., which is proportional to the gel-free .mu. (.mu.0), effective radius (Re), and particle deformability (Fletcher, T. M. et al., 1994). To det. whether the intramol. conformational changes assocd. with salt-dependent chromatin folding influence these electrophoretic parameters, defined ***oligonucleosomes*** were reconstituted from monodisperse tandemly ***repeated*** 5 S DNA and varying amts. of histone octamers. These oligonucleosomes were subjected to both quant. agarose gel electrophoresis and anal. velocity ultracentrifugation in buffers contg. 0-2 mM MgCl2. Ionic conditions that caused a 40% increase in the oligonucleosome sedimentation coeff. (s20,w) also caused both a 30% decrease in Re and a 60% decrease in the magnitude of the .mu.o. Furthermore, the Mg2+-dependent changes in s20,w, Re, and .mu.0 each exhibited the same nonlinear dependence on the degree of nucleosome satn. of the DNA. Thus, quant. agarose gel electrophoresis can be used to detect and characterize the process of chromatin folding. This approach can be used for characterization of the conformational dynamics of many other types of macromol. assemblies, including those systems that are not yet amenable for study by more traditional quant. biophys. techniques.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)

L9 ANSWER 81 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1994:450904 CAPLUS <<LOGINID::20090921>>
DN 121:50904
OREF 121:9022h,9023a
TI A rapid scanning strip for tri- and dinucleotide short tandem repeats
AU Wehnert, Manfred S.; Matson, Robert S.; Rampal, Jang B.; Coassin, Peter J.; Caskey, C. Thomas
CS Dep. Mol. Human Genet., Baylor Coll. Med., Houston, TX, 77030, USA
SO Nucleic Acids Research (1994), 22(9), 1701-4 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB ***Oligonucleotides*** representing 60 trinucleotide (21mers) and four dinucleotide (20mers) tandem ***repeats*** were directly synthesized and arrayed onto an aminated polypropylene substrate. DNA samples of different complexities (a CAG-contg. 21mer oligonucleotide, PCR fragments of 200 to 3000 bp, and cosmids with 31 to 35 kb inserts) were radiolabeled and hybridized to the oligonucleotide ***array*** at various temps. When compared to sequence data available from the test DNAs, the reverse blot system specifically identified various tri- and dinucleotide short tandem repeats (STRs) in every case. Moreover, there was no random or cross hybridization to nonspecific sequences. It was possible to detect as few as 3 repeated units in particular location, as shown for (CCT)n, (GCC)n and (CAC)n triplets in cosmid DNA. Varying the hybridization stringency can enhance the detection of STRs. This single-step reverse blot system therefore allows the rapid, specific and sensitive identification of various STRs in DNA sources of different complexity.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)

L9 ANSWER 82 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1994:155320 CAPLUS <<LOGINID::20090921>>
DN 120:155320
OREF 120:27177a,27180a
TI Transcriptional mapping of the 3' end of the bovine syncytial virus genome
AU Renshaw, Randall W.; Casey, James W.
CS Coll. Vet. Med., Cornell Univ., Ithaca, NY, 14853, USA
SO Journal of Virology (1994), 68(2), 1021-8 CODEN: JOVIAM; ISSN: 0022-538X
DT Journal
LA English
AB The bovine syncytial virus, a member of the retroviral subfamily Spumavirinae, causes a persistent asymptomatic infection in cattle. Nucleotide sequence anal. of the viral genome revealed two overlapping reading frames in the 3' region, traditionally occupied by accessory-function genes in other complex retroviruses. In order to analyze the transcripts from the accessory-gene region, the authors designed ***oligonucleotide*** primers complementary to sequences within the 5' and 3' long terminal ***repeats*** (LTRs) for use with the PCR. Southern blot anal. of amplification products revealed eight major cDNA bands. Eleven distinct cDNA clones were subsequently isolated and characterized. The initial splice donor in each clone is located 49 bp downstream from the mRNA cap site in the 5' LTR. The primary splice acceptor site was located 17 bp upstream from the proximal 3' open reading frame known as BF-ORF1. A second major splice acceptor was localized to a region upstream of the second open reading frame, BF-ORF2. Clones were identified which spliced directly to each of these sites. Addnl. splice donor and acceptor sites within BF-ORF1 and BF-ORF2 and the 3' LTR were variously used to generate a complex ***array*** of multiply spliced transcripts. Each of these transcripts remained in frame and coded for a potential protein product.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L9 ANSWER 83 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1994:97352 CAPLUS <<LOGINID::20090921>>
DN 120:97352
OREF 120:17155a,17158a
TI Pre-germination genotypic screening using PCR amplification of half-seeds
AU Chunwongse, J.; Martin, G. B.; Tanksley, S. D.
CS Dep. Plant Breed. Biometry, Cornell Univ., Ithaca, NY, 14853-1902, USA
SO Theoretical and Applied Genetics (1993), 86(6), 694-8 CODEN: THAGA6; ISSN: 0040-5752
DT Journal
LA English
AB A simple and rapid PCR-based method was developed for detg. the genotype of seeds before germination. Single half-seeds of rice (Oryza sativa) and wheat (Triticum aestivum) were preincubated, without grinding, in an aq. extn. buffer. The resulting supernatants were then used in polymerase chain reaction (PCR) with ***oligonucleotide*** primers corresponding to rice single-copy sequences or a wheat microsatellite ***repeat*** . PCR products of identical size were amplified using either the half-seed ext. or DNA isolated from leaf tissue. The remnant half-seeds can be maintained in ordered ***arrays*** using microtiter plates allowing the recovery of selected genotypes. Pre-germination genotypic screening of seed populations should be useful for a variety of applications in plant breeding and genetics studies.
OSC.G 34 THERE ARE 34 CAPLUS RECORDS THAT CITE THIS RECORD (34 CITINGS)

L9 ANSWER 84 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1993:618902 CAPLUS <<LOGINID::20090921>>

DN 119:218902
OREF 119:38833a,38836a
TI Comparative DNA sequence features in two long Escherichia coli contigs
AU Cardon, Lon R.; Burge, Chris; Schachtel, Gabriel A.; Blaisdell, B. Edwin; Karlin, Samuel
CS Dep. Math., Stanford Univ., Stanford, CA, 94035, USA
SO Nucleic Acids Research (1993), 21(16), 3875-84 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The recent sequencing of two relatively long (approx. 100 kb) contigs of E. coli presents unique opportunities for investigating heterogeneity and genomic organization of the E. coli chromosome. The authors have evaluated a no. of common and contrasting sequence features in the two new contigs with comparisons to all available E. coli sequences (>1.6 Mb). The authors' analyses include assessments of: (i) counts and distributions of restriction sites, special ***oligonucleotides*** (e.g., Chi sites, Dam and Dcm methylase targets), and other marker ***arrays*** ; (ii) significant distant and close direct and inverted ***repeat*** sequences; (iii) sequence similarities between the long contigs and other E. coli sequences; (i.v.) characterization and identification of rare and frequent ***oligonucleotides*** ; (v) compositional biases in short ***oligonucleotides*** ; and (vi) position-dependent fluctuations in sequence compn. The two contigs reveal a no. of distinctive features, including: a cluster of five repeat/dyad elements with very regular spacings resembling a transcription attenuator in one of the contigs; REP elements, ERICs, and other long ***repeats*** ; distinction of the Chi sequence as the most frequent ***oligonucleotide*** ; regions of clustering, overdispersion, and regularity of certain restriction sites and short palindromes; and comparative domains of inhomogeneities in the two long contigs. These and other features are discussed in relation to the organization of the E. coli chromosome.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L9 ANSWER 85 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1993:596970 CAPLUS <<LOGINID::20090921>>
DN 119:196970
OREF 119:34944h,34945a
TI Microsatellites and associated repetitive elements in the sheep genome
AU Buchanan, Fiona C.; Littlejohn, Roger P.; Galloway, Sue M.; Crawford, Allan M.
CS Cent. Gene Res., Univ. Otago, Dunedin, N. Z.
SO Mammalian Genome (1993), 4(5), 258-64 CODEN: MAMGEC; ISSN: 0938-8990
DT Journal
LA English
AB To det. the frequency and clustering of a variety of simple di- and trinucleotide repeats, an Artiodactyl short interspersed element (SINE), an ovine satellite repeat, and a human Alu 1 repeat were used to screen a random selection of cosmids contg. inserts of ovine genomic DNA. In total, 197 individual cosmids were digested with EcoRI and the fragments sepd. on 0.7% agarose gels. Southern blots of these gels were then sequentially probed with (AC)7, (CT)9, and (CAC)6 ***oligonucleotides*** , and the ***repeats*** described above. The frequency at which (AC)n, (CT)n, and (CAC)n repeats were found in the cosmids indicated that they occurred at av. intervals of 65 kb, 367 kb, and 213 kb resp. within the ovine genome. The Artiodactyl SINE was the most common, occurring at an av. interval of 20 kb. No human Alu 1 sequences were detected. There was a significant pos. assocn. between the (AC)n and the Artiodactyl SINE. This assocn. is quite strong as there was significant clustering of the 2 repeats both within cosmids and also within the EcoRI fragments of the digested genomic fragments. With the exception of the sheep satellite sequence, which occurs in tandem ***arrays*** , none of the other repeats showed significant clustering within the 41-kb (av. size) cosmid inserts. The first 25 ovine microsatellites characterized had an av. polymorphic information content (PIC) of 0.65. The different microsatellite types, contg. either perfect, imperfect, or compd. repeats, had similar av. PICs of 0.64, 0.65, and 0.66 resp. There was a weak regression relationship (R2(adj)% = 21.9) between the length of the longest uninterrupted dinucleotide repeat in the largest allele and the PIC of the microsatellite.
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (23 CITINGS)

L9 ANSWER 86 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1993:95235 CAPLUS <<LOGINID::20090921>>
DN 118:95235
OREF 118:16529a,16532a
TI A simple method of detecting amplified DNA with immobilized probes on microtiter wells
AU Kawai, Shintaro; Maekawajiri, Shinji; Yamane, Akio
CS Inst. Biotechnol. Res., Wakunaga Pharm. Co., Ltd., Hiroshima, 729-64, Japan
SO Analytical Biochemistry (1993), 209(1), 63-9 CODEN: ANBCA2; ISSN: 0003-2697
DT Journal
LA English
AB The authors have developed a simple hybridization method for the detection of specific DNA sequences amplified by polymerase chain reaction (PCR). This method is similar to an ELISA format in that labeled PCR products at the 5' termini are hybridized with probes immobilized on a microtiter well and the bound PCR products are detected in a manner similar to that of an enzyme immunoassay (EIA). Two improvements have been made in immobilizing the probe to the microtiter wells, in terms of increasing both immobility and hybridization efficiency. One is that single-stranded (ss) DNA without the complementary strand, is used. The other is that instead of a single copy, a tandem ***array*** of the probe is used for immobilization and hybridization. Use of ssDNA contg. about a 60- ***repeat*** ***array*** of a relevant sequence as an immobilized probe, the sensitivity increased 10-fold over that of a single ***oligonucleotide*** unit. The authors also found that the hybridization conditions such as time, temp., and soln. compn. could be simplified. Therefore this method is esp. suited for handling of a large no. of samples, for example detection of viruses, bacteria, and other pathogens, as well as most human genetic disorders.
OSC.G 33 THERE ARE 33 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)

L9 ANSWER 87 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1992:188711 CAPLUS <<LOGINID::20090921>>
DN 116:188711
OREF 116:31791a,31794a
TI Degenerate ***oligonucleotide*** sequence-directed cross-species PCR cloning of the BCP 54/ALDH 3 cDNA: priming from inverted ***repeats*** and formation of tandem primer ***arrays***
AU Cooper, David L.; Baptist, Edward W.
CS Med. Cent., Duke Univ., Durham, NC, 27710, USA

SO PCR Methods and Applications (1991), 1(1), 57-62 CODEN: PMAPES; ISSN: 1054-9803
DT Journal
LA English
AB Bovine corneal protein 54 (BCP 54) is the major sol. proteins of the bovine cornea, and immunoreactive forms of this protein have been described in a wide range of mammals. Dideoxy sequence detn. of a previously synthesized 420-bp cDNA to BCP 54 generated by the novel mixed oligonucleotide primer amplification of cDNA (MOPAC) procedure revealed extensive similarity to the cDNA encoding tumor-assocd. rat liver (class 3) aldehyde dehydrogenase (RATALD). PCR amplification with addnl. pairs of degenerate oligonucleotide sequence (DOS) primers derived from both BCP 54-amino-acid sequence and amino acid and nucleotide sequence data from RATALD produced three PCR products that were cloned and subsequently sequenced. The major product was 716-bp BCP 54 cDNA clone encompassing the BCP 54 carboxy-terminal amino acid sequence for which the DOS pair was designed. Sequence alignment of the BCP 54 cDNA and its translation product with RATALD demonstrated 81% and 85% identity at the nucleotide and amino acid levels, resp. Anal. of the addnl. two clones established that they were the results of PCR artifactual processes. The first of these was a 552-bp product occurring at elevated primer concns. that formed through bidirectional amplification from a single DOS annealing to an inverted repeat located in the BCP 54 coding sequence. The second artifactual product was a 212-bp sequence that contained several unreported amplification anomalies, including the formation of a tandem primer ***array*** .
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L9 ANSWER 88 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1990:114324 CAPLUS <<LOGINID::20090921>>
DN 112:114324
OREF 112:19259a,19262a
TI Monovalent cation-induced structure of telomeric DNA: the G-quartet model
AU Williamson, James R.; Raghuraman, M. K.; Cech, Thomas R.
CS Howard Hughes Med. Inst., Univ. Colorado, Boulder, CO, 80309, USA
SO Cell (Cambridge, MA, United States) (1989), 59(5), 871-80 CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB Structures formed by ***oligonucleotides*** composed of 2 or 4 ***repeats*** of the telomeric sequences from Oxytricha and Tetrahymena were investigated. The Oxytricha 4-repeat mol. [d(T4G4)4 = Oxy-4] forms structures with increased electrophoretic mobility in nondenaturing gels contg. Na+, K+, or Cs+, but not in gels contg. Li+ or no added salt. Formation of the folded structure results in protection of a set of dG's from methylation by di-Me sulfate. Efficient UV-induced crosslinks are obsd. in Oxy-4 and the related sequence from Tetrahymena [d(T2G4)4 = Tet-4], and join thymidines in different repeats. Models proposed to account for these data involve G-quartets, H-bonded structures formed from 4 guanosines in a square-planar ***array*** . It is proposed that the G-quartet structure must be dealt with in vivo by the telomere replication machinery.
OSC.G 430 THERE ARE 430 CAPLUS RECORDS THAT CITE THIS RECORD (434 CITINGS)

L9 ANSWER 89 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1986:1574 CAPLUS <<LOGINID::20090921>>
DN 104:1574
OREF 104:291a,294a
TI Interspersed repeats in mammalian DNAs: a status report
AU Schmid, Carl W.; Paulson, K. Eric
CS Dep. Chem., Univ. California, Davis, CA, 95616, USA
SO Genet.: New Front., Proc. Int. Congr., 15th (1984), Meeting Date 1983, Volume 1, 255-67. Editor(s): Chopra, V. L. Publisher: Oxford IBH Publishing Co., New Delhi, India. CODEN: 54GNAQ
DT Conference
LA English
AB The structures of 3 families of interspersed repeats found in mammalian DNAs was examd. Each is flanked by short direct repeats which are usually preceded by an A-rich genomic sequence. Members of each family usually terminate in essentially a polyadenylated 3' end. Alu Family members are usually full-length representatives of a single consensus sequence. Kpn Family members show variable and extensive truncations of the 5' end of the sequence. O family members differ by an internal insertion of addnl. sequence. Each of these distinct families is probably dispersed by way of an RNA intermediate. A 2nd major group of interspersed ***repeats*** consists of tandem ***arrays*** of simple ***oligonucleotides*** , such as CA. Regardless of whether interspersed repeats have a biol. function, their abundance, widespread genomic distribution, and mobility guarantees that they will have important genetic effects.

L9 ANSWER 90 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1983:449099 CAPLUS <<LOGINID::20090921>>
DN 99:49099
OREF 99:7619a,7622a
TI Cleavage of chromatin with methidiumpropyl-EDTA.cntdot.iron(II)
AU Cartwright, Iain L.; Hertzberg, Robert P.; Dervan, Peter B.; Elgin, Sarah C. R.
CS Dep. Biol., Washington Univ., St. Louis, MO, 63130, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1983), 80(11), 3213-17 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Methidiumpropyl-EDTA.cntdot.Fe(II) (I) cleaves double-helical DNA with considerably lower sequence specificity than micrococcal nuclease. The patterns generated from the 1.688 g/cm3 complex satellite DNA-contg. chromatin 5 S rRNA and histone gene sequences of Drosophila melanogaster chromatin, and protein-free DNA by I and micrococcal nuclease cleavage were compared. I, at low concns., recognizes the nucleosome ***array*** , efficiently introducing a regular series of single-stranded (and some double-stranded) cleavages in chromatin DNA. Subsequent S1 nuclease digestion of the purified DNA produces a typical extended ***oligonucleosome*** pattern, with a ***repeating*** unit of .apprx.190 base pairs. Under suitable conditions, relatively little other nicking is obsd. Unlike micrococcal nuclease, which has a noticeable sequence preference in introducing cleavages, I cleaves protein-free tandemly repetitive satellite and 5 S DNA sequences in a near-random fashion. The spacing of cleavage sites in chromatin, however, bears a direct relation to the length of the resp. sequence repeats. In the case of the histone gene sequences, a faint, but detectable, I cleavage pattern is obsd. on DNA, in some regions similar to and in some regions different from the strong chromatin-specified pattern. I will be very useful in the anal. of chromatin structure.
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (29 CITINGS)

L9 ANSWER 91 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1983:120555 CAPLUS <<LOGINID::20090921>>
DN 98:120555
OREF 98:18277a,18280a
TI Properties of a polymorphic DNA segment in the 5' flanking region of the human insulin gene
AU Bell, Graeme I.; Karam, John H.; Rutter, William J.
CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA
SO Progress in Clinical and Biological Research (1982), 103(Hum. Genet., Pt. A), 57-65 CODEN: PCBRD2; ISSN: 0361-7742
DT Journal
LA English
AB The 5' flanking region of the human insulin [9004-10-8] gene displays length and sequence variability. This polymorphic region begins 363 base pairs (bp) from the 5' end of the gene and extends upstream for a variable distance. The restriction fragment length heterogeneity is generated by variation in the redundancy of a family of 14-15-bp GC-rich oligonucleotides. The most frequent sequence for this family is ACAGGGGTGTGGGG. The DNA sequence heterogeneity is produced by differences in the arrangement of members of this ***oligonucleotide*** family within the tandemly ***repeating*** ***array*** . The function of the polymorphic region is unknown.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

L9 ANSWER 92 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1983:102067 CAPLUS <<LOGINID::20090921>>
DN 98:102067
OREF 98:15477a,15480a
TI Definition of the simian virus 40 early promoter region and demonstration of a host range bias in the enhancement effect of the simian virus 40 72-base-pair repeat
AU Byrne, Barry J.; Davis, Mark S.; Yamaguchi, Julie; Bergsma, Derk J.; Subramanian, Kiranur N.
CS Health Sci. Cent., Univ. Illinois, Chicago, IL, 60612, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1983), 80(3), 721-5 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The simian virus 40 (SV40) origin region includes the viral replication origin and the early and late promoters and consists of a few palindromes, a 17-base-pair (bp) adenine + thymine-rich sequence, 3 copies of a guanine + cytosine-rich 21-bp repeat, and 2 copies of a 72-bp repeat. Sequential deletions were made in the SV40 origin region, and the early promoter efficiencies of these truncated DNA segments were detd. by connecting them in the correct orientation with the coding regions of selectable marker genes and assaying the expression of the chimeric marker genes in vivo in different host cell lines. A truncated SV40 early promoter segment contg. only the TATA box and the major in vivo mRNA initiation sites has essentially no promoter efficiency. The major component of the SV40 early promoter was located within the 21-bp ***repeated*** sequences, which consist of an alternating and mutually overlapping ***array*** of 2 cytosine-rich ***oligonucleotides*** having the consensus sequences Y-Y-C-C-G-C-C-C (Y = pyrimidine nucleoside) and G-C-C-C-(C)-T/A-A/T-A/(T)-C-T. One-2 copies of the 21-bp repeat were adequate for gene expression under conditions in which the enhancement effect of the 72-bp repeat was minimal. The SV40 72-bp repeat exhibits a pronounced host range in its enhancement of gene expression; the enhancement is only 2-fold in nonpermissive mouse cells but amts. to 10- or 20-fold in permissive monkey cells or semipermissive human cells, resp.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L9 ANSWER 93 OF 93 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1978:418557 CAPLUS <<LOGINID::20090921>>
DN 89:18557
OREF 89:2875a,2878a
TI The nucleotide sequence of oocyte 5S DNA in Xenopus laevis. I. The AT-rich spacer
AU Fedoroff, Nina V.; Brown, Donald D.
CS Dep. Embryol., Carnegie Inst. Washington, Baltimore, MD, USA
SO Cell (Cambridge, MA, United States) (1978), 13(4), 701-16 CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB The primary sequence of the principal spacer region in X. laevis oocyte 5 S DNA was detd. The spacer is AT-rich and comprises .gtoreq.50% of each repeating unit. The sequence is internally repetitious. The spacer, which varies in length from .apprx.360 to .gtoreq.570 nucleotides, is subdivided into a region (A2) which is variable in length in different repeating units, flanked by regions (A1, A3, B1) which are relatively const. in length. The A2 region consists, on the av., of 5-6 tandem copies of the ***oligonucleotide*** CAAAGTTT-GAGTTTT; variation in the redundancy of this ***oligonucleotide*** accounts for much of the ***repeat*** length variation in genomic 5 S DNA. Most copies of this oligonucleotide are identical. Regions A1 and A3 comprise a linear ***array*** of similar, but not identical, ***oligonucleotides*** ; most ***repeating*** units contain very similar A1 and A3 sequences. Region B1 is a sequence of 49 nucleotides immediately adjacent to the 5' terminus of the 5 S rRNA sequence. It is (guanine + cytosine)-rich, much less repetitive than the remainder of the spacer, and contains several palindromes, but no regions of dyad symmetry. This sequence is identical in all 6 of the single cloned repeating units of 5 S DNA analyzed.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

=> d his
(FILE 'HOME' ENTERED AT 19:19:56 ON 21 SEP 2009)
FILE 'CAPLUS' ENTERED AT 19:20:27 ON 21 SEP 2009
L1 271500 S (ARRAY# OR MICROARRAY#)/BI,AB
L2 2485 S ((DUPLICAT? OR REPLICAT? OR REPEAT?)(30A)((OLIGO(W)NUCLE?) OR
L3 234 S L1 AND L2
L4 213 S L3 NOT 2009/PY
L5 181 S L4 NOT 2008/PY
L6 153 S L5 NOT 2007/PY
L7 127 S L6 NOT 2006/PY
L8 111 S L7 NOT 2005/PY
L9 93 S L8 NOT 2004/PY

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